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Sequence 30, Appl
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Fatent No. 6794136

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: JAMIESON, Andrew

APPLICANT: JAMIESON, Andrew

APPLICANT: REBAR, Edward

TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING

TITLE OF INVENTION: PROTEINS

FILE REPERENCE: 325-6020

CURRENT FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PALENTIN VEr. 2.0

SEQ ID NO 30

LENGTH: 7
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                                                                                                                                December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29.197 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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Score Match Length DB
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Perfect score:
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TYPE: PRT ORGANISM: Artificial Sequence FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: VEGF-II US-09-716-637-30
                                                                    Query Match 100.0%; Score 7; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Word size :

Searched:

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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sugamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT PAPLICANTION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 15
LENGTH: 99
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APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Javvis, Eric Edward
APPLICANT: Javvis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
FILE REFERENCE: 019496-0022003
CURRENT APPLICATION NUMBER: US/09/229,037A
                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F2
US-09-716-637-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: VEGF1 OTHER INFORMATION: construct targeting upstream 9-base pair OTHER INFORMATION: site in VEGF promoter
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CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SEQ TWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 7
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Sequence 17,
Sequence 3, A
Sequence 5, A
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Sequence 18,
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APPLICANT: LIU, Qiang
APPLICANT: LAW, Qiang
APPLICANT: AMMESON, Andrew
APPLICANT: REBAR, Edward
TITLE OF INVENTION: TERRATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
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... /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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... /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
... /cgn2_6/ptodata/1/iaa/BTTTS_COMB.pep:*
... /cgn2_6/ptodata/1/iaa/PGTTS_COMB.pep:*
... /cgn2_6/ptodata/1/iaa/PGTTS_COMB.pep:*
                                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-229-037-15
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US-09-478-681-30
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Gapop 60.0 , Gapext 60.0
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Patent No. 6794136
GENERAL INFORMATION:
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Maximum DB seq length: 200000000
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                                                       Copyright
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TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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    NUMBER OF SEQ ID NOS: 43
                   SOFTWARE: Patentin Ver.
SEQ ID NO 17
LENGTH: 99
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GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Byratt, Sharon K.

TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZINC FINGER PROTEINS

FILE REFERENCE: 8325-0002.10 / S2-US3

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT PILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

ILENGTH: 99
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APPLICANT: Cox III, George N.
APPLICANT: Case, Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stric E.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REPRENCE: 8325-0002.10 / $2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: VEGF3a ZFP OTHER INFORMATION: construct targeting downstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP; OTHER INFORMATION: construct targeting upstream 9-base pair target ; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
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US-03-478-681-15
Sequence 15, Application US/09478681
; Partent No. 6607882
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Patent No. 6607882
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
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                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-478-681-17
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; OTHER INFORMATION: Description of Artificial Sequence:VEGF3a ZFP; OTHER INFORMATION: construct targeting downstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-17
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US-09-779-233-5
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US-09-779-233-3
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                                                                                            DB 4;
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100.0%; Pred. No. 1.3;
iive 0; Mismatches
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APPLICANT: Case, Casey,
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REPERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 99
                                                                                          Query Match 100.0%; Score 7; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 7; Conservative 0; Mismatches
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US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
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Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                               US-09-229-037-30

IS-09-229-037-30

Sequence 30, Application US/09229037A

Sequence 30, Application US/09229037A

Patent No. 6534261

APPLICANT: Case, Casey Christopher

APPLICANT: Eisenberg, Stephen P.

APPLICANT: Sardamo Biosciences, Inc.

TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using

TITLE OF INVENTION: Angulation of Endogenous Frice Repression in Cells Using

TITLE OF INVENTION: 21nc Finger Proteins

FILE REFERENCE: 019496-002200US

CURRENT APPLICANT: 1999-01-12

NUMBER OF SEQ ID NOS: 40

SOFTWARE PATENTING DATE: 1999-01-12

SOFTWARE PATENTING DATE: 1999-01-12
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Jarvis, Eric E.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: WEGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 8325-0002.10 / S2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence:designed OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 6607882
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53 RSSNLOR 59
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US-09-478-681-30
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TYPE: PRT
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Gaps
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100.0%; Pred. No. 2.4;
Live 0; Mismatches
US-09-719-233-18

Sequence 18, Application US/09779233

Sequence 18, Application US/09779233

Patent No. 6689558

PAPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REFERENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 18
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Job time : 15.9 secs
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ORGANISM: Artificial Sequence
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Gaps

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Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Database :

Result No.

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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Stephen P.
APPLICANT: Steenberg, Stephen P.
APPLICANT: Steenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
APPLICANTON WUMBER: Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION WUMBER: US/09/229,037A
CURRENT APPLICATION WUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
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Patent No. 6534261
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Snagamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-00220008
CURRENT APPLICATION NUMBER: US/09/229,037A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP OTHER INFORMATION: construct targeting upstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 7; DB 4; Length 99; 100.0%; Pred. No. 1.3;
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Best Local Similarity 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/716,637 CURRENT FILING DATE: 2001-10-12 NUMBER OF SEQ ID NOS: 35 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 7; Conser
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                                                                                                                                                                                            December 27, 2004, 18:12:11; Search time 15:9 Seconds (without alignments) 29:197 Million cell updates/sec
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Sequence 15,
Sequence 17,
Sequence 3, A
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Sequence 30,
Sequence 30,
Sequence 18,
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APPLICANT: JAMIESON, Andrew
APPLICANT: JAMIESON, Andrew
APPLICANT: REBAR, Edward
TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
PILE REFERENCE: 8325-0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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/cgn2_6/ptodata/1/iaa/sB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/sB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/sB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/sB_CTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-229-037-15
US-09-229-037-17
US-09-478-681-15
US-09-779-233-3
US-09-779-233-3
US-09-229-037-30
US-09-279-037-30
US-09-779-233-5
US-09-779-233-5
US-09-779-233-5
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Gapop 60.0 , Gapext 60.0
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Patent No. 6794136
GENERAL INFORMATION:
APPLICANT: EISENBERG, Stephen P.
                                                                                                                                                                                                                                                                                            US-09-846-033B-72
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Maximum DB seq length: 200000000
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Match Length
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OTHER INFORMATION: Description of Artificial Sequence:VEGF3a ZFP OTHER INFORMATION: construct targeting downstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
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US-09-779-233-5
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US-09-779-233-3
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100.0%; Pred. No. 1.3;
rative 0; Mismatches
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100.0%; Pred. No. 1.3;
ative 0; Mismatches
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Patent No. 668958
GENERAL INCRMATION:
APPLICANT Case, Casey
TITLE OF INVENTION:
FILE REFERENCE: 8325-0010
CURRENT APPLICANTION NUMBER: US/09/779,233
CURRENT FILING DATE: 201-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Case, Casey,
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REPERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
LENGTH: 99
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18-09-779-233-3
1 Sequence 3, Application US/09779233
1 Patent No. 6689558
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ORGANISM: Artificial Sequence
                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 99
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-779-233-5
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LENGTH: 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Spratt, Sharon K.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REPERENCE: 8325-0002.10 / S2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 99
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Sequence 17, Application US/09478681

Patent No. 6607882

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: NSGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 8125-0002.10 / S2-US3

CURRENT APPLICATION UNMER: US/09/478,681

CURRENT FILING DATE: 2000-01-06
                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: VEGF3a ZFP A. OTHER INFORMATION: construct targeting downstream 9-base pair target CTHER INFORMATION: site in VEGF promoter US-09-229-037-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
OTHER INFORMATION: construct targeting upstream 9-base pair target
OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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; Sequence 15, Application US/09478681
; Patent No. 6607882
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SCFTWARE: PALENLIN VEY. 2.0
SEQ ID NO 17
LENGTH: 99
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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53 RSSNLOR 59
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Jarvis, Eric Edward
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
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US-09-478-681-30

Sequence 30, Application US/09478681

Patent No. 6607882

APPLICANT: Case, Casey Christopher

APPLICANT: Case, Casey Christopher

APPLICANT: Spratt, Sharon K.

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REGILATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZINC FINGER PROTEINS

FILE REFERENCE: 8325-0002.10 / S2-US3

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 196

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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                      RESULT 8
US-09-229-037-30
Sequence 30, Application US/09229037A
Parent No. 6534261
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
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53 RSSNLQR 59
53 RSSNLOR 59
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US-09-779-233-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 196;
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                                                                            RESULT 10
8-09-779-233-18
5 Sequence 18, Application US/09779233
Fatent No. 668958
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILICANTION DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
LENGTH: 196
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ORGANISM: Artificial Sequence
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53 RSSNLQR 59
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Perfect score:

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Sequence:

Scoring table:

Word size :

Searched:

Database :

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APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Case, Casey C.
APPLICANT: Jamieson, Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Bangamo Biosciences, Inc.
APPLICANT: Broteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
FILE REPERENCE: 1999-01-12
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 94
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:phage display; OTHER INFORMATION: selected and mutagenized
US-09-494-190-69
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                                                                                                                                                                                                                                                                                                                                                  Sequence 69 Application US/09494190

Sequence 6.0 Application US/09494190

SENERAL INFORMATION:

APPLICANT: BARBAS, CARLOB F.

TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN FILE REFERENCE: TSRI 645.2

CURRENT APPLICATION NUMBER: US/09/494,190

CURRENT APPLICATION NUMBER: EP/99/07742

PRIOR FILING DATE: 1999-10-14

PRIOR FILING DATE: 1999-10-16

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PATENTIN VET: 2.1
                                                                        Query Match
100.0%; Score 7; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
; OTHER INFORMATION: codon binding sequence US-09-173-941-69
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
7; Conserve
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US-09-494-190-69
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                                                                                                                                                                                      December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29:197 Million cell updates/sec
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TITLE CO INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN FILE REFERENCE: NOVO081S
CURRENT APPLICATION NUMBER: US/09/173,941
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEC ID NOS: 120
SOFTWARE: PATCHIN Ver. 2.1
SEC ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgm2_6/prodata/1/iaa/5A_COMB.pep:*
/cgm2_6/prodata/11iaa/5B_COMB.pep:*
/cgm2_6/prodata/1/iaa/6A_COMB.pep:*
/cgm2_6/prodata/11iaa/6B_COMB.pep:*
/cgm2_6/prodata/11iaa/PCTUS_COMB.pep:*
/cgm2_6/prodata/11iaa/PCTUS_COMB.pep:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-494-190-69
US-09-229-007A-94
US-10-113-424-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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                                                                                                                                         OM protein - protein search, using sw model
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ORGANISM: Artificial Sequence
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Maximum DB seq length: 200000000
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Match Length DB
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0; Indels Length 7;

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Sequence 94, Application US/10113424

Sequence 94, Application US/10113424

Patent No. 6785613

(GENERAL INFORMATION:
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Case, C.
APPLICANT: Gos, II, George N.
APPLICANT: Gos, III, George N.
APPLICANT: Sandamo Blosciences, Inc.
APPLICANT: Sandamo Blosciences, 
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OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence
CTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223
US-10-113-424-94
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Best Local Similarity 100.0%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 7; Conservative 0; Mismatches 0; Indels
Query Match
100.0%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 7; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Sequence 21, Application US/09731558

Patent No. 6503717

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Babar, Edward J.
APPLICANT: Rebar, Edward J.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT PILING DATE: 2000-12-06
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN VEV. 2.1
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                                                                                                                                      December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29.197 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                            OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Score Match Length DB
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US-09-731-558-21
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Perfect score:
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LENGTH: 7
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Sequence 21, Application US/09731558

Patent No. 6503717

GENERAL INFORMATION:

APPLICANT: Gase, Casey Christopher

APPLICANT: Gase, Casey Christopher

APPLICANT: Bangame Bloscience, Inc.

APPLICANT: Rebar, Edward J.

APPLICANT: Rebar, Edward J.

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019496-003210US

FILE REFERENCE: 019496-003210US

CURRENT FILING DATE: 1200-12-06

PRIOR APPLICATION NUMBER: US/09/731,558

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                    December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29:197 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Score Match Length DB
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LENGTH: 7
TYPE: PRT
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; ORGANISM: Artificial Sequence; FRATURE:
; PRATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SBS10
; OTHER INFORMATION: recognition helix
US-09-731-558-21

Query Match

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps Qy

| QSGNLAR 7
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Job time: 15.9 secs
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0; Indels

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Database :

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Sequence 29, Application US/09716637

Sequence 29, Application US/09716637

Sequence 29, Application US/09716637

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: APPLICANT: Admission, Andrew

APPLICANT: REBAR, Edward

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix
                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:SBS3; OTHER INFORMATION: recognition helix US-09-731-558-14
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100.0%; Pred. No. 3.8e+05;
iive 0; Mismatches 0;
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Fatent No. 669958
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION:
FILE REPRENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779, 233
CURRENT APPLICATION NUMBER: US/09/779, 233
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                   NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
TENGTH.
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Matches 7; Conserv
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1 RSDHLSR 7
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US-09-779-233-44
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LENGTH: 7
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Sequence 29, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 18, Appl
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Sequence 14, Application US/09731558
Patent No. 6503717
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Preteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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(c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-49
US-09-229-037-15
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-779-233-18
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Maximum DB seq length: 200000000
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US-09-229-037-30

US-09-229-037-30

Squence 30, Application US/09229037A

Patent No. 6534261

GENERAL INFORMATION:

APPLICANT: Cox III, George No. 6534261bert

APPLICANT: Eisenberg, Stephen P.

APPLICANT: Spratt, Sharon Kaye

APPLICANT: Spratt, Sharon Kaye

APPLICANT: Spratt, Sharon Raye

APPLICANT: Spratt, Sharon Raye

APPLICANT: Spratt, Sharon Raye

TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using

TITLE OF INVENTION: Line Finger Proteins

TITLE OF INVENTION: 2inc Finger Proteins

TILE REFERENCE: 019496-002200US

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ 1D NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ 1D NO 3
LENGTH: 99
                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       US-09-779-233-3
; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 7; Conservative 0,
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                                                                                                                                                          Conservative
                                                                              Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                      81 RSDHLSR 87
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Sequence 15, Application US/09229037A

Sequence 15, Application US/09229037A

PERENT NO. 6534261

APPLICANT: Case, Casey Christopher

APPLICANT: Senherg, Stephen F.

APPLICANT: Spratt, Sharon Kaye

APPLICANT: Spratt, Sharon Kaye

APPLICANT: Spratt, Sharon Kaye

APPLICANT: Spratt, Sharon Kaye

APPLICANT: Spratt Company Company

TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using

FILE REFERENCE: 019496-0022000S

CURRENT APPLICATION NUMBER: US/09/229,037A

CURRENT APPLICATION NUMBER: US/09/229,037A

SOFTWARE: Patentin Ver. 2.0
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Sequence 15, Application US/09478681

Sequence 15, Application Case, Casey Christopher

APPLICANT: Case, Casey Christopher

APPLICANT: Gast, Casey Christopher

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REGILATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZING FINGER PROTEINS

FILE REFERENCE: 8325-0002.10 / S2-US3

CURRENT PAPLICATION NUMBER: US/09/478,681

CURRENT PILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 43

SOOTWARE: PatentIn Ver. 2.0
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                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP OTHER INFORMATION: construct targeting upstream 9-base pair target : OTHER INFORMATION: site in VEGF promoter US-09-229-037-15
                               ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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                                                                                                                                                          0; Indels
                                                                                                        Length 7;
                                                                                                        100.0%; Score 7; DB 4; L6 100.0%; Pred. No. 3.8e+05;
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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81 RSDHLSR 87
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1 RSDHLSR 7
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LENGTH: 99
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LENGTH: 99
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                       RESULT 8

US-09-478-681-30

; Sequence 30, Application US/09478681
; Patent No. 6607882
; General INFORMATION:
; APPLICANT: Case, Casey Christopher
APPLICANT: Esemberg, Stephen P.
; APPLICANT: Spratt, Sharon K.
; TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
; TITLE OF INVENTION: USING ZING ZING STORE
; TITLE OF LIANG DATE: 2000-11-06
; UNMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
LENGTH: 196
; TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233
Fatent No. 6689558
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION:
FILE REPERENCE: 8325-0010
CURRENT APPLICATION WUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
LENGTH: 196
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ORGANISM: Artificial Sequence
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| 178 RSDHLSR 184
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178 RSDHLSR 184
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Sequence 16, Application US/09731558

Sequence 16, Application US/09731558

Patent No. 650317

GENERAL INFORMATION:

APPLICANT: Case, Case
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                                                                                                                                                                                                                                                        December 27, 2004, 18:12:11; Search time 15:9 Seconds (without alignments) 29:197 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 4 US-09-731-558-16
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Gapop 60.0 , Gapext 60.0
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Score Match Length DB
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LENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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; ORGANISM: Artificial Sequence; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SBS5
; OTHER INFORMATION: recognition helix
US-09-731-558-16
Query Match
Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 QSGSLTR 7
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Db 1 QSGSLTR 7
Search completed: December 27, 2004, 19:21:22
Job time: 15.9 secs
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OTHER INFORMATION: Description of Artificial Sequence: Zinc finger; OTHER INFORMATION: peptide
US-09-424-487B-11
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Patent No. 6007988
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fillsbury Madison & Sutro, L.L.P.
                                                                                  PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:SBS9
OTHER INFORMATION: recognition helix
US-09-731-558-20
                                                                                                                                                                                         100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; Pred. No. 3.8e+05; Attive 0; Mismatches 0; Indels
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APPLICANT: CHOO, YEN
APPLICANT: KUG, AARON
APPLICANT: SALAN, WARK
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
FILE REFERENCE: 71278/264975
CURRENT APPLICATION NUMBER: US/09/424,487B
CURRENT FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: GB 9710809.6
PRIOR APPLICATION NUMBER: POT/GB98/01512
PRIOR APPLICATION NUMBER: POT/GB98/01512
PRIOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New York Avenue, N.W.
STATE: D.C.
COUNTRY: USA
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; Sequence 11, Application US/09424487B
; Patent No. 674683B
                                            TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                       Query Match
Best Local Similarity 100.
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COMPUTER READABLE FORM:
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12 DRSNLTR 18
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LENGTH: 27
SEQ ID NO 20
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                        LENGTH:
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Sequence 20, Application US/09731558

Patent No. 650377

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Edward J.

APPLICANT: Sangamo Biodecences, Inc.

TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019496-003210US

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT FILING DATE: 2000-12-06

PRIOR PRING DATE: 1999-12-06

NUMBER: OF SEQ ID NOS: 24-12-06
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                                                                                                                                                      December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29.197 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, 1
Sequence 11, 1
Sequence 18, 1
Sequence 18, 2
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-424-487B-11
US-08-793-408-18
US-09-139-762A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                              478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                      Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                  US-09-846-033B-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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89
89
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Perfect score:
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Database :

No. Result

Word size

Searched:

Sequence:

Run on:

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Gaps

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Sequence 18, Application US/09139762A
Fatent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Sanchez Garcia, Isidro
APPLICANT: Sanchez Garcia, Isidro
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillabury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2005-3918
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: IBM PC Compatible
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/09/139,762A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,408
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 942534.9
FILING DATE: 08-NOV-1994
FILING DATE: 08-NOV-1994
FILING DATE: 08-NOV-1994
FILING DATE: 20-AUG-1994
FILING DATE: 80-NOC-1994
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CLASETE CATION:
PRICE APPLICATION:
PRICE APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UNI 1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
FILING DATE: 17-AUG-1995
FILING DATE: 17-AUG-1995
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-793-408-18
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pRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9422534.9

FILING DATE: 08-NOV-1994

PRIOR APPLICATION NATA:

PRIOR APPLICATION NUMBER: GB 9416880.4

FILING DATE: 20-AGU-1994

INFORMATION FOR SEQ ID No: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 89 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: protein

US-09-139-762A-18

Query Match

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 7; Conservative 0; Mismatches 0; Indels

Qy 1 DRSNLTR 7

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| DB 74 DRSNLTR 7

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| DB 74 DRSNLTR 80

Search completed: December 27, 2004, 19:21:22
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Gaps

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Scoring table:

Word size :

Searched:

Database :

Result

Perfect score:

Title:

Run on:

Sequence:

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OTHER INFORMATION: Description of Artificial Sequence: Zinc finger OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Choo, Yen
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                              TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:SBS9
OTHER INFORMATION: recognition helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 7; DB 4; Length 27; Best Local Similarity 100.0%; Pred. No. 0.064; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              100.0%; Score 7; DB 4; Length 7;
100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-424-487B-11
Sequence 11, Application US/09424487B
Sequence 11, Application US/09424487B
Sequence 11, Application US/09424487B
Setent No. 6746838
GENERAL INFORMATION:
APPLICANT: CHOO, YEN
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
CURRENT APPLICATION NUMBER: US/09/424,487B
CURRENT FILING DATE: 1997-05-23
PRIOR FILING DATE: 1997-05-23
PRIOR PILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 12
SEQ ID NO 11
SEC ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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ZIP: 20005-3918
COMPUTER READABLE FORM:
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US-08-793-408-18
                                                                                                                                                                                  US-09-731-558-20
SEQ ID NO 20
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APPLICANT: Gase, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Proteins for the Identification of Gene Function
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 2000-12-06
PRIOR PILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                             (without alignments)
29.197 Million cell updates/sec
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Sequence 11, A
Sequence 18, A
Sequence 18, A
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                                                                                                                                                                                  December 27, 2004, 18:12:11 ; Search time 15.9 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-424-487B-11
US-08-793-408-18
US-09-139-762A-18
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Gapop 60.0 , Gapext 60.0
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; Sequence 20, Application US/09731558
Patent No. 6503717
; GENERAL INFORMATION:
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Maximum DB seq length: 2000000000
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Match Length DB
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74 DRSNLTR 80
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; Sequence 18, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
APPLICANT: Choo, Yean
APPLICANT: Sanchez Garcia, Isidro
ITILE OF INVENTION: Improvements in or Relating to
ITILE OF INVENTION: Improvements in or Relating to
ITILE OF INVENTION: Improvements in or Relating to
ITILE OF INVENTION: Indiang Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
COUNTRY: USA
STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
COMPUTER: Nord Perfect
COMPUTER: USA
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
FILING PAREN
FILING PAREN
FILING PAREN
FILING PAREN
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FILING PAREN
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,408
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 08-NOV-1994
FILING DATE: 08-NOV-1994
FILING DATE: 20-AUG-1994
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 0.2 US 08/793,408
FILING DATE: 17-AUG-1997
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-793-408-18
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74 DRSNLTR 80
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 942534.9
FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994

INPORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 18:

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-139-762A-18

Query Match

Best Local Similarity 100.0%; Score 7; DB 3; Length 89;

MAtches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 DRSNLTR 7

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| Db 74 DRSNLTR 80

Search completed: December 27, 2004, 19:21:22
Job time: 16.9 secs
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Gaps

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0; Indels Length

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Zinc finger
COTHER INFORMATION: peptide
US-09-424-487B-10
                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-00-793-408-18
i Sequence 18, Application US/08793408
j Patent No. 6007988
j Patent No. 700, Yan
j APPLICANT: Church Yan
j APPLICANT: Sanchez Garcia, Isidro
j TITLE OF INVENTION: Improvements in or Relating to
j TITLE OF INVENTION: Binding Proteins for Recognition of DNA
j NUMBER OF SEQUENCES: 18
j CORRESPONDENCE ADDRESS:
j ADDRESSE: Plilsbury Madison & Sutro, L.L.P.
street: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 7; DB 3;
100.0%; Pred. No. 0.1;
:ive 0; Mismatches
                                                                                                                                                                  100.0%; Score 7; DB 4;
100.0%; Pred. No. 0.035;
Ative 0; Mismatches 0
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: GB-08-NOV-1994
PRIOR APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
FILING DATE: 20-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,408
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                      TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: amino acid
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Best Local Similarity 100.
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 28
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                                                                                                                                                  December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29.197 Million cell updates/sec
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Sequence 18, P
Sequence 18, A
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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; Batent No. 6746838
; GENERAL INFORMATION:
    APPLICANT: CHOO, YEN
; APPLICANT: KLUG, AARON
; APPLICANT: KLUG, AARON
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
; TITLE REFERENCE: 71278/264975
; CURRENT APPLICATION NUMBER: US/09/424,487B
; CURRENT PILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: GB 9710809.6
; PRIOR FILING DATE: 1997-05-23
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-424-487B-10
US-08-793-408-18
US-09-139-762A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               478139 segs, 66318000 residues
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                            Title:
Perfect score:
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Word size :

Searched:

Sequence:

Run on:

Database :

Result

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Gaps

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Length 89; 0; Indels

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Geogene 18, Application US/09139762A

Sequence 18, Application US/09139762A

SEQUENCES TREET IN TALE OF INVENTION: Improvements in or Relating to TITLE OF INVENTION: Indiang Proteins for Recognition of DNA NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS: 125

CORRESPONDENCE PAILBBURY Madison & Sutro, L.L.P.

STATE: 100 New York Avenue, N.W.

STATE: 1100 New York Avenue, N.W.

CONTRY: USA

CONTRY

CONTRY
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Query Match 100.0%; Score 7; DB 3; Length 89; Best Local Similarity 100.0%; Pred. No. 0.1; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 DRSHLTR 7

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Db 46 DRSHLTR 52

Search completed: December 27, 2004, 19:21:21 Job time : 15.9 secs

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TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
RSDHLTT 7
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US-09-614-679A-19
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Sequence 1, Appli
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                                                                                                       December 27, 2004, 18:12:11; Search time 15:9 Seconds (without alignments) 29:197 Million cell updates/sec
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Sequence 1, Al
Sequence 70, 7
Sequence 7, Al
Sequence 7, Al
Sequence 7, Al
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-466-344-8
US-08-863-813A-5
US-08-676-318A-5
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                                                                             - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                          Word size :
                                                                                OM protein
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Patent No. 5206152
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Sequence 2, A
Sequence 2, A
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Sequence 36,
Sequence 44,
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Sequence 8,
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APPLICANT: Choo, Yen
APPLICANT: Ranchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
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Sequence
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US-09-614-679A-19
                                                                              Sequence
                                                                                                                   Sequence
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100.0%; Pred. No. 3.8e+05;
ive 0; Mismatches 0;
US-09-500-700-5
US-08-224-482-11
US-08-863-813A-34
US-08-676-318A-36
US-09-500-700-34
US-09-500-700-34
US-09-500-700-34
US-09-500-700-36
US-09-500-700-36
US-09-500-700-36
US-09-500-700-36
US-09-500-700-44
US-09-538-092-1278
US-09-234-482-8
US-08-24-482-6
US-08-24-482-6
US-08-24-482-6
US-08-24-482-6
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US-08-24-482-6
US-08-24-482-6
US-08-24-66-348-2
US-08-24-66-348-2
US-08-24-69-36-2
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APPLICANT: BATEL, SACHIN
APPLICANT: BALSUBRAMANIAN, SHANKAR
APPLICANT: BLASUBRAMANIAN, SHANKAR
APPLICANT: LIU, XIAOHAI
APPLICANT: LIU, XIAOHAI
TILE REFERENCE: 71278/271599
CURRENT APPLICATION NUMBER: US/09/614,679A
CURRENT FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
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Patent No. 6492117
GENERAL INFORMATION:
APPLICANT: CHOO, YEN
APPLICANT: PATEL, SACHIN
APPLICANT: BALASUBRAMANIAN, SHANKAR
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Gaps
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Patent No. 5763209
GENERAL INPORMATION:
APPLICANT SUKhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS NUMBER OF SEQUENCES: 67
CORRESPONDENCES. 67
CORRESPONDENCES. Arnold, White & Durkee
STREET: 321 No. 5763209th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 7; DB 3; Length 10; 100.0%; Pred. No. 0.017; Atrive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 08-NOV.1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ 1D NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REGISTRANCON TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 321 NO. 5763209th Clark St CITY: Chicago STATE: 111inois COUNTRY: U.S.A. ZIP: 60610 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (112) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 19:
SEQUINNE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv...
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-139-762A-53
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APPLICANT: Choo, Yen
APPLICANT: Choo, Yen
APPLICANT: Study, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 7; DB 3; Length 10; 100.0%; Pred. No. 0.017; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
PILING DATE: 03-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
PILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
BROUGHOUS CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
                                 ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILING DATE:
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ZIP: 2005-3918
COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,7627
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-139-762A-53
; Sequence 53, Application US/09139762A
; Patent No. 6013453
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Best Local Similarity 100.
Matches 7; Conservative
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FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
LENGTH: 21
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.,
Local 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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Patent No. 6453242
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Jamieson, Andrew
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Pangamo Biosciences, Inc.
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STAFF: Illinois
CONTRY: U.S.A.
ZIP: 60610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COUGHLIA, DATA:
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: 36,111
REFERENCE/DOCKET NUMBER: 36,111
REFERENCE/DOCKET NUMBER: 36,111
REFERENCE/DOCKET NUMBER: 36,111
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0.
                                                                                                                                                                                       US-08-466-344-19; Sequence 19, Application US/08466344; Patent No. 5773583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (312) 744-0090
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Best Local Similarity 100.
Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-466-344-19
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9 RSDHLTT 15
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                                      RSDHLTT 7
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RESULT 7

US-10-113-424-95

US-10-113-424-95

Sequence 95, Application US/10113424

Patent No. 6785613

GENERAL INFORMATION:
PAPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Bebar. Beward.
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger FILE REFERENCE: 019496-001800US

TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger FILE REFERENCE: 019496-001800US

CURRENT APPLICATION NUMBER: US/09/229,007A

PRIOR PILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 97

SEQ ID NO 95

LEMOTH: 21

FANDER OF SEQ ID NOS: 21

SEQ ID NO 95

LEMOTH: 21

FANDER OF SEQ ID NOS: 21

FANDER OF SEQ ID NOS: 21
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US-10-113-424-95
CTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-09-229-007A-95
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Patent No. 5928955
GENERAL INFORMATION:
APPLICANT: Imperiali, Barbara
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 7; DB 4; Length 21; 100.0%; Pred. No. 0.033; tive 0; Mismatches 0; IndelB
                                                                                                                   Length 21;
                                                                                                                   100.0%; Score 7; DB 4; Length 21;
100.0%; Pred. No. 0.033;
tive 0; Mismatches 0; Indels
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RESULT 10

RESULT 10

RESULT 10

Sequence 34, Application US/08466344

Sequence 34, Application US/08466344

Sequence 34, Application US/08466344

Sequence 34, Application US/08466344

SERENAL INFORMATION:
TITLE OF INVENTION: WETHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: PUNCTIONAL DOMAINS OF DNA BINDING PROTEINS UNMERS OF SEQUENCES: 67

CORRESPONDENCES: 67

STATE: 11110018

COMPUTER: 111100
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                                                                                                                                                                                                                                                                                                                                       100.0%; Score 7; DB 1; Length 28; 100.0%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 28 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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STRANDEDNESS: si
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US-08-040-548-34
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US-09-058-459-1
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| Sequence 34, Application US/08040548
| Sequence 34, Application US/08040548
| Patent No. 5763209
| GENERAL INFORMATION:
| APPLICANT: SUKhatme, Vikas P. TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: WINCTIONAL DOMAINS OF DNA BINDING PROTEINS NUMBER OF SEQUENCES: 67
| CORRESPONDENCE ADDRESS: ADDRESSE: ATNOIG, White & Durkee STREET: 321 No. 5763209th Clark Street, Suite 800 CITY: Chicago STATE: Illinois COUNTRY: U.S.A. ZIP: 60610
| COMPUTER: EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
| CURRENT APPLICATION DATE: US/08/040,548
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ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Tloppy disk
COMPUTER: Datentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,151
FILING DATE: 22-MAR-1996
CLLASSIFICATION: A22
ATTORNEY/ACENT INFORMATION:
NAME: Shannon, Karen L.
REFERENCE/DOCKET NUMBER: 356,675
REFERENCE/DOCKET NUMBER: 356,675
REFERENCE/ADOCKET NUMBER: 356,675
TELECOMMUNICATION NUMBER: 312-321-4290
TELEFAM: 312-321-4299
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LEMBOTH: 26 amino acids
TTPE: amino acids
TTPE: ATTORNEY/ACENTERISTICS:
LEMBOTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-151-111
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1 RSDHLTT 7
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APPLICANT: Dahiyat, Bassil L.
APPLICANT: Gordon, D. Benjamin
APPLICANT: Gordon, D. Benjamin
APPLICANT: Gordon, D. Benjamin
APPLICANT: Su, Yaoying
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION NUMBER: 60/054,678
PRIOR FILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
PRIOR APPLICATION NUMBER: 60/061,097
PRIOR APPLICATION NUMBER: 60/087,561
PRIOR APPLICATION NUMBER: 09/059,561
PRIOR APPLICATION NUMBER: 06/087,561
                                                                                        APPLICANT: Mayo, Stephen L.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Gordon, D. B.
APPLICANT: Gordon, D. B.
APPLICANT: Street, Arthur
TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
FILE REFERENCE: A65383-3/RFT/RMS/SJR
CURRENT FILING DATE: 1097-04-11
PRIOR APPLICATION NUMBER: 60/044,678
PRIOR APPLICATION NUMBER: 60/054,678
PRIOR PILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 7; DB 3; Length 28; Best Local Similarity 100.0%; Pred. No. 0.043; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09127926
Patent No. 6269312
GENERAL INFORMATION:
Sequence 1, Application US/09058459
Patent No. 6188965
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Mouse
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ORGANISM: Mouse
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14 RSDHLTT 20

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APPLICANT: Greisman, Harvey A.
APPLICANT: Greisman, Harvey A.
APPLICANT: Greisman, Harvey A.
APPLICANT: Greisman, Harvey A.
APPLICANT: Pabo, Carl O.
INTILE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc
TITLE OF INVENTION: Finger Proteins for Diverse DNA Target Sites
FILE REFERENCE: 019496-000220US
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 60/073,223
EARLIER APPLICATION NUMBER: US 60/073,223
SOFTHARE: PatentIn Ver. 2.0
SOFTHARE: PatentIn Ver. 2.0
SEC ID NO 2
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                          APPLICANT: BULLETE, JETY
APPLICANT: BULLETE, JETY
APPLICANT: Haber, Daniel A.
APPLICANT: Haber, Daniel A.
APPLICANT: Housman, David B.
APPLICANT: Bruening, Wendy
APPLICANT: Bruening, Wendy
APPLICANT: Bruening, Wendy
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
TITLE OF INVENTION: Wilms' Tumor Gene
TITLE OF INVENTION: WINBER: US/09/037,179B
CURRENT APPLICATION NUMBER: US/09/037,179B
CURRENT FILING DATE: 1998-03-09
PRIOR FILING DATE: 1993-08-0.
PRIOR APPLICATION NUMBER: US 07/415,161
PRIOR PILING DATE: 1999-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR PILING DATE: 1994-10-13
PRIOR PILING DATE: 1994-10-13
PRIOR PILING DATE: 1994-09-27
NUMBER OF SEC ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 3; Length 28; 100.0%; Pred. No. 0.043; cive 0; Mismatches 0; Indels
Sequence 15, Application US/09037179B Patent No. 6316599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-240-179-2
'Sequence 2, Application US/09240179
'Patent No. 6410248
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                                                                                    APPLICANT: Call, Katherine M. APPLICANT: Glaser, Thomas M. APPLICANT: Ito, Caryn Y. APPLICANT: Buckler, Alan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
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ORGANISM: Homo sapien
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US-09-714-357-1
; Sequence 1, Application US/09714357
; Patent No. 6708120
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Street, Arthur
; TITLE OF INVENITON: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; TILE REFERENCE: A65353-3/RFT/RMS/SJR
; CURRENT PILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1997-08-04
; PRIOR FILING DATE: 1997-08-04
; PRIOR PELING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
                                            0; Gaps
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Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels
Query Match
100.0%; Score 7; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                            14 RSDHLTT 20
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; ORGANISM: Mouse
US-09-714-357-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proceins for the Identification of Gene Function
TITLE OF INVENTION: Proceins for the Identification of Gene Function
TITLE OF INVENTION: Proceins for the Identification of Gene Function
TITLE OF INVENTION: Proceins for the Identification of Gene Function
TITLE OF INVENTION NUMBER: US/09/731,558
CURRENT FILING DATE: 1999-12-06
FRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOSTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                              December 27, 2004, 18:12:11 ; Search time 15.9 Seconds (without alignments) 29:197 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      478139 segs, 66318000 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                  US-09-846-033B-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Score Match Length DB
                                                                                                                                                                                                                                                                                                       1 RSDALTR 7
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Perfect score:
Sequence:
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LENGTH: 7
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
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                                                                                                                                                      Run on:
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8
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p ORGANISM: Artificial Sequence
preparing:
preparing:
property Reservation of Artificial Sequence: SBS1
corner in Corner in Description of Artificial Sequence: SBS1
corner in Corner in 100.0%; Score 7; DB 4; Length 7;
guery Match
Best Local Similarity 100.0%; Fred. No. 3 8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDALTR 7
bb 1 RSDALTR 7
Corner in Search completed: December 27, 2004, 19:21:20
Corner in Search completed: December 27, 2004, 19:21:20
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TYPE: PRT
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Sequence 19, Application US/09731558

Patent No. 6503717

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Case, Casey Christopher

APPLICANT: Bangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019496-003210US

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT FILING DATE: 1999-12-06

MUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Appl
Sequence 32, Appl
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                                                                                                                                      December 27, 2004, 17:02:31 ; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
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1: /cgn2_6/ptodatea1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodatea1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-731-558-19
US-09-716-637-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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US-09-731-558-19
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-716-637-32
US-09-716-637-32
; Sequence 32, Application US/09716637
; Patent No. 6794136
; GENERAL INFORMATION:
; APPLICANT: EISENBERG, Stephen P.
; APPLICANT: LIU, Olang
APPLICANT: LIU, Olang
; APPLICANT: REARR, Marard
; TITLE OF INVENTION: PROTEINS
; TITLE OF SEQ ID NOS: 35
; SEQ ID NO 32
; LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Description of Artificial Sequence: VEGF-IV F1
US-09-716-637-32
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                                                             CTHER INFORMATION: Description of Artificial Sequence:SBS8 OTHER INFORMATION: recognition helix US-09-731-558-19
                                                                                                                                                         Query Match

100.0%; Score 7; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; rive 0; Mismatches 0; Indels
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 7; Conservative
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Homo sapiens.
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37.620 Million cell updates/sec
                                                                                                         December 27, 2004, 17:02:30 ; Search time 66.75 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                  70
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                              2002273 segs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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geneseqp2003as:*
geneseqp2003bs:*
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geneseqp1990s:*
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Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.	CLICAROLLO
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Description	6 Zinc	4 Zinc	7 Zinc	0 Zinc	029 Zinc	6 Zinc	134 Zinc	7 Zinc	6 Zinc	Abp48398 Zinc fing			Aab47802 VEGF-1 zi	Abj03904 Human VEG	Abj03800 Human VEG	Abj03802 Human VEG	Abj03801 Human VEG	Aae30448 VEGF spec	Abo01200 Human VEG	Abo01097 Human VEG	Abo01096 Human VEG	Human	Abol4460 Human VEG	Abol4461 Human VEG	Abol4462 Human VEG
ID	ABP49026	ABP48774	ABP48777	ABP48780	ABP49029	ABP48396	ABP49134	ABP48397	ABP49056	ABP48398	ABB07125	AAB47808	AAB47802	ABJ03904	ABJ03800	ABJ03802	ABJ03801	AAE30448	AB001200	ABO01097	ABO01096	ABO01098	ABO14460	ABO14461	AB014462
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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	_	Ada62760 Zinc fing	Ada62844 Zinc fing	Ada62879 Zinc fing		Ada62759 Zinc fing	Ada62224 Zinc fing	_		Ada62853 Zinc fing	Adm21047 Synthetic	Adm21057 Synthetic		Adm21048 Synthetic	Adm20426 Synthetic	Adm20964 Synthetic	Adm20428 Synthetic	Adm20427 Synthetic	Adm21083 Synthetic	
6 ABO14564	7 ADA62761	7 ADA62760	7 ADA62844	7 ADA62879	7 ADA62222	7 ADA62759	7 ADA62224	7 ADA62223	7 ADA62843	7 ADA62853.	7 ADM21047	7 ADM21057	7 ADM20965	7 ADM21048	7 ADM20426	7 ADM20964	7 ADM20428	7 ADM20427	7 ADM21083	
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26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45	

ALIGNMENTS

New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus. Zinc finger protein; ZFP; DNA binding protein; zinc finger. Zinc finger protein related peptide motif SEQ ID NO:814. ABP49026 ID ABP49026 standard; peptide; 7 AA. (SANG-) SANGAMO BIOSCIENCES INC. 20-NOV-2001; 2001WO-US043438. 20-NOV-2000; 2000US-00716637. 28-AUG-2002 (first entry) WPI; 2002-500284/53. WO200242459-A2. 30-MAY-2002. Liu Q;

Example 1; Page 45; 81pp; English

The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (M); (2) a polymuclecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S4 target subsite, thus designing (I) that binds to he S4 target subsite, thus designing (I) that binds to he S4 target subsite, thus designing (I) that binds to he S4 target subsite that it binds to the S6 target subsite of the subsite such that it binds to the S6 target subsite of the subsite such that it binds to the S6 target subsite sharing the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant

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The present invention describes a zinc finger protein (I) that binds to a carget site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3.5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (S1) carget subsite, as electing the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the H8 starget site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5' most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant conginate the expression of a target region within a subject, in modulate the expression of a target region within a subject, in a sample, and in assays to determined the phenotype and function of in a sample.
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engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity, ABQ71213 to ABQ72214 and ABP48191 to ABP5130 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         engineering, comprises N- to C-terminus.
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                                                                                                                                                                                                                                   DB 5; Le
1.7e+06;
                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                   Score 7;
Pred. No.
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100.0%;
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) and cainc finger, ordered FT, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CT) comprising (I); (2) a polyhucleotide (III) encoding (I) or (II); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it that it binds to the S3 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to the tit binds to the S3 target subsite, thus designing (I) that binds to useful in studying gene function, and for human therapeutic and plant engineering (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of an assays to determined biological activity ABG71213 to target sequences, as well as enhanced biological activity ABG71213 to ABG72214 and ABB78191 to ABB78210 represent in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
gene expression. (1) has improved affinity and specificity for their target sequences, as well as enhanced biological activity, ABQ12131 to ABQ72214 and ABP48191 to ABG51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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100.0%; Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                           ABP48777 standard; peptide; 7 AA.
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0; Indels Length 7;

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Zinc finger protein, ZFP, DNA binding protein; zinc finger.
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100.0%; Score 7; DB 5; Le
100.0%; Pred. No. 1.7e+06;
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          Query Match
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                                                                                                                                                 100.0%; Score 7; DB 5; Length 7; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zinc finger protein related peptide motif SEQ ID NO:732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP48780 standard; peptide; 7 AA
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                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                    Sequence 7 AA;
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                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP48780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) inc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the carget site comprises, in 3.-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it compacts to the S1 target subsite, and selecting the F3 zinc finger such that it compacts to the S1 target subsite, and selecting the F3 zinc finger such that it compacts to the S1 target subsite, thus designing (I) that binds to the S1 target subsite, thus designing (I) that binds to the S1 target subsite, and selecting the F3 zinc finger such that it compacts to the S1 target subsite, thus designing (I) that binds to the S1 target subsite, and for human therapeutics and plant considering (I) (II) or (III) is useful in studying gene function, and for human therapeutics and plant companies for sequence specific detection of target nucleic acid adaptostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression (I) has improved affinity and specificity for their carget sequences, as well as enhanced biological activity. AB071213 to target sequences and zinc function of the present continuant to the part of the present continuant on the part of the present continuant of the present continuant of the present continuant of the present contents and plant of the present co
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New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
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                                                                                                                                                                                                                                                                                           Example 1; Page 45; 81pp; English.
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Best Local Similarity 100.
Matches 7; Conservative
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Sequence 7 AA;

(first entry)

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ABP49134 standard; peptide; 7 AA.
                                                                                              28-AUG-2002
                                                                  ABP49134;
                        ABP4913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a zinc finger protein (1) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) and carrier site, comprising a first (F1), a second (F2), and a third (F3) are carrier site to comprises, in 3'-5' firom N-terminus to C-terminus, where the carget site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (I1) comprising (I1); (2) a polymuclectide (I11) encoding (I) or (I1); and (I) involves selecting the F1 zinc finger such that it binds to the S2 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites are such a target site. (I) is useful for recognition of the subsite. (I) is useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in modulate the expression of a target region within a subject, in a sample, and in assays to determined the phenotype and function of in a sample, and in assays to determined the phenotype and function of the expression. (I) has improved affinity and specificity for their carriers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. AB071213 to AB072214 and ABP48191 to ABP21210 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
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                                                                                                                                                                                    Zinc finger protein related peptide motif SEQ ID NO:193.
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                                                                                                 ABP48396 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                           (SANG-) SANGAMO BIOSCIENCES INC.
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Best Local Similarity
Matches 7; Conserv
TTSNLRR 7
                   TTSNLRR
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                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                          28-AUG-2002
                                                                                                                                                                                                                                                                                                                      30-MAY-2002.
                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                            ABP48396;
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) condered F1, F2, F3 from N-terminus to C-terminus, where the carget site comprises, in 3'-5' direction, a first (SI), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CI) comprising (I); (2) a polyfuncleotide (III) encoding (I) or (II); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it comparison (I) is useful for recognition of triplet target subsites that it binds to the S3 target subsite, thus designing (I) that binds to the S1 target subsite, thus designing (I) that binds to the S1 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of the subsites of a target site (II) is useful in therapeutic methods to useful in studying gene function, and for human therapeutic and plant endiance (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. ABQ11213 to ABQ72214 and ABB78131 to ABB72130 represent in the expresent
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                                                                 Zinc finger protein; ZFP; DNA binding protein; zinc finger.
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Zinc finger protein related peptide motif SEQ ID NO:850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 46; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANG-) SANGAMO BIOSCIENCES INC.
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Best Local Similarity 100.
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                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                        Synthetic.
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                                                               Zinc finger protein related peptide motif SEQ ID NO:194.
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100.0%; Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                 (SANG-) SANGAMO BIOSCIENCES INC.
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                                         (first entry)
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                           WO200242459-A2.
                                                                                                                      Homo sapiens.
                                       28-AUG-2002
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                                                                                                                                  Synthetic.
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               ABP48397;
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carget site, comprising a first (F1), a second (F2), and a third (F3) carget site, comprising a first (F1), a second (F2), and a third (F3) cainc finger, ordered F1, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (I1) comprising (I); (2) a polymotleotide (III) encoding (I) or (III); and (S2) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it that it binds to the S3 target subsite, thus designing (I) that binds to the S1 target subsite, and selecting the F3 zinc finger such that it carget site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutic and plant condulate the expression of a target region within a subject, in city sequence specific detection of target nucleor acid cin a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. AB071213 to AB072214 and AB0748191 to AB072214 and Specific appresent DNA target sequences, as well as enhanced biological activity. AB071213 cinvention
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                                                                     Zinc finger protein; ZFP; DNA binding protein; zinc finger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
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Zinc finger protein related peptide motif SEQ ID NO:824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 7; DB 5; Le
100.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 45; 81pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2000; 2000US-00716637.
                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2001; 2001WO-US043438.
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les 7; Conserv
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                                                                                                                                                                                                                                                               WO200242459-A2.
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                                                                                                                                                  Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                    30-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Modification of chromatin structure for facilitating transcription, replication and repair, comprises contacting chromatin with fusion molecule comprising DNA binding domain and component of a chromatin
                                                                                                                                                                                                                                                                                                               Example 1; Page 59; 99pp; English.
                                                                                                                                                      (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                           28-APR-2000; 2000US-0200590P.
28-AUG-2000; 2000US-0228523P.
                                                                                 27-APR-2001; 2001WO-US040616
                                                                                                                                                                                  Collingwood T;
                                                                                                                                                                                                             WPI; 2002-075165/10.
                                                                                                                                                                                                                                                                                     remodeling complex
                          WO200183793-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF-A protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
Homo sapiens.
                                                     08-NOV-2001
                                                                                                                                                                                  Wolffe AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB47808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXX
                                                                                                                                                                                                                                                                                                                                    The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2) and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (G1), a second (G2), and a third (G3) target subsite. Also described are: (I) a polypeptide (C1) comprising (I); (2) a polyfuclectide (III) encoding (I) or (II); and (C1) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it compress to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S1 target subsite, and selecting of F4 F3 zinc finger such that it compress to the S3 target subsite, thus designing (I) that binds to the S1 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (C1) a target selection of triplet carget subsites (C2) modulate the expression of a target region within a subject, in charge technical carget sequences, as well as enhanced biological activity. ABG71213 to CASG72214 and ABG72214 and ABG72214 and ABG72214 or the exemplification of the present carget in the present carget peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                   New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF; chromatin; cytostatic; vasotropic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; anti-HIV; antisickling; neuroprotective; nootropic; cerebroprotective; antibacterial; fungicide; virucide; gene therapy; Veg 1; zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 7; DB 5; Length 7; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                              Example 1; Page 38; 81pp; English.
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                                                                                                                                                                     (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                         20-NOV-2000; 2000US-00716637.
                                                                                                             20-NOV-2001; 2001WO-US043438
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                                                      WO200242459-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2002
                                                                                  30-MAY-2002
                          Synthetic.
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                                                                                                                                                                                                 Liu O;
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The invention provides a method of modifying a region of interest in cellular chromatin that involves contacting the cellular chromatin with a cellular chromatin that involves contacting the cellular chromatin with a cellular chromatin that involves contacting the cellular chromatin with a cellular chromatin molecule comprises a DNA binding domain and a component of a chromatin remodeling complex or its functional fragment, which complexes the region of interest. The method is useful for modifying a region of interest. The method is useful for modifying a region of interest. The method is useful for modifying a region of interest correctivated receptor (PPAR-gamma2), pl6, p53, pRb, dystrophin and e-cadebrain in cellular chromatin present in a plant, animal or human cell. The chromatin modification facilitates detection of sequence of interest comprising a single nucleotide polymorphism, cativation or repression of a gene of interest or recombination between an exogenous nucleic acid and cellular chromatin. It also results in generation of an accessible region in the cellular chromatin which carefulating expression of a gene and for binding an exogenous molecule to prophylactic groove binders and intercalators. The fusion molecule may be used for modulating expression of a gene and for binding an exogenous molecule to prophylactic comply to modulate gene expression, for therapeutic or prophylactic complications, e.g., for treating cancer, ischemia, diabetic retinopathy, sickle cell anemia, Alzheimer's disease, muscular degeneration, rheumatoid arthritis, psoriasis, HIV infection, infectious fungus, e.g., chlamydia, Mycobacteria, Pneumococci, infectious fungus, e.g., chlamydia, Mycobacteria, Pneumococci, infectious fungus, e.g., chlamydia, Mycobacteria, Pneumococci, infectious fungus, e.g., chlamydia, psoriasis, e.g., ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Matches 7; Conservative
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VEGF-1 zinc finger domain F4.

25-MAR-2002 (first entry)

AAB47802;

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The sequences given in AAB47802-16 represent zinc finger domains derived from transcriptional effector proteins. These transcriptional effector proteins. These transcriptional effector proteins. These transcriptional effector transcriptional initiation site of the human vascular endothelial growth factor (VEGF) gene. Target site #1 was bound by a binding domain containing six zinc fingers, named VEGF31/1. Target site #2 was bound by a three-finger zinc finger domain, VEGF-1, and a control six-finger domain, GATA 15.5, was designed to bind to target sequence #3. The zinc finger containing proteins were used to demonstrate the method of the invention for binding an exception molecule (EM) to a binding site (BS), where the BS is located within a region of interest in cellular chromatin. The method comprises identifying an accessible region within the accessible region, and introducing the EM into the cell, where the EM binds site in cellular chromatin for modulating gene expression by administering an exogenous molecule. The binding of an exogenous molecule contained and site site of containing site in cellular chromatin can be used for detection of a particular sequence, for example, an exogenous molecule, such as a sequence-specific DNA binding protein, can be used to detect variant alleles associated with a disease or with a particular phenotype in the presence of pathological microoraganisms in colinical processions molecule.
                                                   Target site; transcriptional effector protein; zinc finger domain; human; vascular endothelial growth factor; VEGF; cellular chromatin; gene expression; sequence-specific; DNA binding protein; phenotype; copy number; p53; cancer; gene function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding an exogenous molecule (EM) to a binding site located within a region of interest in chromatin, useful for modulating gene expression, by identifying an EM target site within an accessible region and introducing the EM into the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Page 25; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 Case CC;
                                                                                                                                                                                                                                                                                                                                                                                       (SANG-) SANGAMO BIOSCIENCES INC.
                    VEGF3a/1 zinc finger domain F4.
                                                                                                                                                                                                                                                                                                                                            28-APR-2000; 2000US-0200590P.
                                                                                                                                                                                                                                                                                                 27-APR-2001; 2001WO-US013631
                                                                                                                                                                                                                                                                                                                                                                                                                                 Raschke E, Wolffe AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-066534/09
                                                                                                                                                                                                              WO200183751-A2.
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                                                                                                                                                                                                                                                       08-NOV-2001
                                                                                                                                                                      Synthetic
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in clinical samples. Exogenous molecules can also be used to quantify copy number of a gene in a sample. For example, detection of the loss of one copy of a p53 gene in a clinical sample is an indicator of susceptibility to cancer. The methods can also be used in assays to determine gene function and to determine changes in phenotype resulting from specific modulation of gene expression
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Gaps
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0
100.0%; Score 7; DB 5; Length 7; 100.0%; Pred. No. 1.7e+06;
                          0; Indels
                          0; Mismatches
                             7; Conservative
  Query Match
Best Local Similarity
                                                      TTSNLRR 7
                             Matches
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TTSNLRR TTSNLRR

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AAB47802 standard; peptide; 7 AA.
RESULT 13
                     AAB47802
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TTSNLRR 7

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The sequences given in AAB47802-16 represent zinc finger domains derived from transcriptional effector proteins. These transcriptional effector proteins. These transcriptional effector proteins were designed to bind to target sites derived from the transcriptional initiation site el was bound by a binding domain of factor (VEGF) gene. Target site #1 was bound by a binding domain containing six zinc finger domain, VEGF2a/1. Target site #2 was bound by a three-finger zinc finger domain, VEGF2a/1. Target site #2 was bound by containing proteins were used to demonstrate the method of the invention for binding an exogenous molecule (EM) to a binding site (BS), where the BS is located within a region of interest in callular chromatin. The method comprises identifying an accessible region within the accessible region of interest, identifying a target site for the EM within the chromatin to the BS. The method is useful for modulating gene expression by administed to the BS. The method is useful for modulating gene expression by administering an exogenous molecule. The binding of an exogenous molecule contained to detect the presence of pathological microorganisms and laless associated with a disease or with a particular spendles and to detect the presence of pathological microorganisms of copy number of a gene in a sample. For example, detection of the loss of copy number of a gene in a sample. For example, detection of the loss of copy number of a gene in a sample. For example, detection of the loss of copy number of a gene in a clinical sample is an indicator of concer. The methods can also be used to quantify for eacestibility to cancer. The methods can also be used to genetic production and to detect the presence of pathological microorganisms determined entaining gene function and to detect the presence of pathological microorganisms determined entaining gene function and to determine the sample of the
                                                                                                                                                         Target site; transcriptional effector protein; zinc finger domain; human; vascular endothelial growth factor; VEGF; cellular chromatin; gene expression; sequence-specific; DNA binding protein; phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Binding an exogenous molecule (EM) to a binding site located within a region of interest in chromatin, useful for modulating gene expression, by identifying an EM target site within an accessible region and introducing the EM into the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 1.7e+06;
:ive 0; Mismatches 0;
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                                                                                                                                                                                                                                   number; p53; cancer; gene function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 25; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANG-) SANGAMO BIOSCIENCES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolffe AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-066534/09.
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                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raschke E,
                                                                                                                                                                                                                                                                                    Synthetic.
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Matches
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Search completed: December 27, 2004, 18:06:48
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Best Local Similarity
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                                                                                                                                                                                                                                                                             Jarvis E;
                                                                                                                                                                                                                                                               Rebar E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or ulcer.
                                                                                                                                                                                      vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention
                                                                                                                                                    Zinc finger protein; angiogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasctropic; antiarthritic; vulnerar antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
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diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth;
                                                                                                                         Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 161.
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                              ABJ03904 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2000; 2000US-00733604.
12-DEC-2000; 2000US-00736083.
30-APR-2001; 2001US-00846033.
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                                                                                            (first entry)
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                                                                                            25-SEP-2002
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Jarvis E;
                                                             ABJ03904;
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RESULT 14
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New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or ulcer.
gene therapy, antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antiulcer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating anglogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischemaia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention
                                                                                                                                                                                                                                                                                                                      Eisenberg SP;
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llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      Liu Q, Liu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 102; 195pp; English.
                                                                                                                                                                                                                                                                                    (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                 06-DEC-2001; 2001WO-US046861.
                                                                                                                                                                                                                  07-DEC-2000; 2000US-00733604.
                                                                                                                                                                                                                                12-DEC-2000; 2000US-00736083.
30-APR-2001; 2001US-00846033.
                                                                                                                                                                                                                                                                                                                      Jamieson A,
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                                                                                                               WO200246412-A2.
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                                                                               Homo sapiens
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Gaps

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Perfect score:

Run on:

Sequence:

Scoring table:

Word Bize :

Searched:

Database :

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GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Stratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Gase, Casey Christopher
APPLICANT: Gase, Stephen P.
APPLICANT: Spratt, Sharon K.
APPLICANT: Spratt, Sharon K.
ITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 3325-0002.10 / $2-US3
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-229-037-15
                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F1
US-09-716-637-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 99;
                                                                                                                                                                                 100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; ative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.91;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
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; Sequence 15, Application US/09478681
; Patent No. 6607882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                ORGANISM: Artificial Sequence FEATURE:
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 7
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
7; Conserv?
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LENGTH: 99
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Sequence 15, Appl
Sequence 3, Appli
Sequence 30, Appli
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Sequence 30, Appl
Sequence 18, Appl
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Fatent No. 6794136
Fatent No. 6794136
FABERAL INFORMATION:
APPLICANT: EISBNBERG, Stephen P.
APPLICANT: LIU, Olang
APPLICANT: JAMIESON, Andrew
APPLICANT: ALLO, TITLE OF INVENTION: ITERATURE OPTIMIZATION IN THE DESIGN OF BINDING
ITLE OF INVENTION: PROTEINS
FILE REPERBNCE: 8125-0020
CURRENT APPLICANTION NUMBER: US/09/716,637
CURRENT FILING DATE: 2011-10-12
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                              .; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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US-09-229-037-15
US-09-478-681-15
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-779-233-18
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                                                                                                                                                    December 27, 2004, 17:02:31
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                                                                                                           OM protein - protein search, using
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Maximum DB seq length: 200000000
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Match Length DB
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TYPE: PRT ORGANISM: Artificial Sequence
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7; Conservative
Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Sequence 30, Application US/09229037A

Patent No. 6534261

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaya
APPLICANT: Spratt, Sharon Kaya
APPLICANT: Spratt, Sharon Kaya
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Regulation of Endogenous
FILE REFRENCE: 019496-002200US
CURRENT PRILIG DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 30

LENGTH: 196

LENGTH: 196
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; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VEGF1
OTHER INFORMATION: construct targeting upstream 9-base pair
OTHER INFORMATION: site in VEGF promoter
                                                                                                                                                          100.0%; Score 7; DB 4; Length 99;
100.0%; Pred. No. 0.91;
iive 0; Mismatches 0; Indels
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Patent No. 668958
GENERAL INFORMATION:
GENERAL TINFORMATION:
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE PATENT Ver. 2.0
SEQ ID NO 3
LENGTH: 99
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ORGANISM: Artificial Sequence
FEATURE:
    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 7; Conservative
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Matches 7; Conservative
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US-09-229-037-30
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US-09-478-681-15
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US-09-779-233-3
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US-09-478-681-30
is Sequence 30, Application US/09478681
is Patent No. 6607882
is GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Bisenberg, State E.
is APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
CURRENT APPLICATION NUMBER: US/09/478,681
is CURRENT FILING DATE: 2000-01-06
is NUMBER OF SEQ ID NOS: 43
is SOFTWARE: PatentIN Ver. 2.0
is SEQ ID NO 30
is LENGTH: 196
is THE CASE OF THE C
                                                                                                    Gaps
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100.0%; Score 7; DB 4; Length 196; 100.0%; Pred. No. 1.6;
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100.0%; Pred. No. 1.6;
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Fatent No. 668958
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICANTS 825-0010
CURRENT APPLICANTON 1001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE PATENTIN VIVE: 2001-02-08
SOFTWARE PATENTIN VE: 2.0
SEQ ID NO 18
LENGTH: 196
                                                                                               0; Mismatches
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Sequence 15.

Sequence 15.

Sequence 15.

Sequence 16.

Sequence 16.

Sequence 16.

Sequence 17.

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                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: VEGF-I
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100.0%; Pred. No. 3.8e+05;
ive 0; Mismatches 0;
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APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Baravia, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
ITILE OF INVENTION: Regulation of Endogenous (TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 01945-000US
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SSOFTWARE: PatentIn Ver. 2.0
SEQ TO NO. 15
LENGTH: 99
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Patent No. 6534261
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                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 7
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Best Local Similarity 100...
7; Conservative
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US-09-229-037-15
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Patent No. 6794136

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: LIU, Olang

APPLICANT: JAMIESON, Andrew

APPLICANT: MEBRA, Edward

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: BASS-0020

CURRENT APPLICATION NUMBER: US/09/716,637

CURRENT FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                                   December 27, 2004, 17:02:31 ; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
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Sequence 15, P
Sequence 3, Ag
Sequence 30, P
Sequence 30, P
Sequence 18, P
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 2000000000
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7; Conservative
Query Match
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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; Sequence 30, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
; APPLICANT: Cox II, George No. 6534261bert
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Zinc Finger Proteins
; FILE REFERENCE: 019496-00220008
; FILE REFERENCE: 019496-00220008
; CURRENT APPLICATION NUMBER: US/09/229,037A
; NUMBER OF SEQ ID NOS: 199-01-12
; NUMBER OF SEQ ID NOS: 200
; SEQ ID NOS 30
; LENGTH: 196
; TYPE: PRT
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                                                                   OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP OTHER INFORMATION: construct targeting upstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
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US-09-779-233-3
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100.0%; Score 7; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 7; Conservative 0; Mismatches 0; Indels
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APPLICANT: Case, Casey
TITLE OF INVENTION:
FILE REPERENCE: 8325-0010
CURRENT APPLICATION UNMER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 99
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Patent No. 6689558
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-229-037-30
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US-09-779-233-3
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Length 196
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 DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/09779233;
Patent No. 668958;
GENERAL INFORMATION:
APPLICANT: Case, Casey,
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY;
FILE REFERENCE: 825-0010;
CURRENT PAPLICATION NUMBER: US/09/779,233;
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 18
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Title: Perfect score:

Sequence:

Scoring table:

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cax III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Stratt, Sharon Kaye
APPLICANT: Saraon Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REPERENCE: 109496-002200US
CURRENT APPLICANT: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 99
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Standary, Stephen P.
APPLICANT: Jarvis, Bric B.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 8325-0002.10 / S2-UG3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-229-037-15
                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F1
US-09-716-637-27
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                                                                                                                                                                                                                                     100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; artive 0; Mismatches 0; Indels
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; Sequence 15, Application US/09229037A
; Patent No. 6534261
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                                                                                  TYPE: PRT ORGANISM: Artificial Seguence
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 27 LENGTH: 7
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                      FEATURE:
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Sequence 15, Appl
Sequence 3, Appli
Sequence 30, Appli
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                                                                                                                                                                                          December 27, 2004, 17:02:31; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
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Sequence 18,
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Patent No. 6794136

GENERAL INCORMATION:
APPLICANT: EIGENBERG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: LAMIESON, Andrew
APPLICANT: REBAR, Edward
TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-229-037-15

US-09-779-233-3

US-09-779-233-3

US-09-478-681-30

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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Best Local Similarity 100...
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120 TISNLRR 126
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US-09-478-681-30
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Sequence 30, Application US/09229037A

Patent No. 6534261

GENERAL INFORMATION:

APPLICANT: Cox II, George No. 6534261bert

APPLICANT: Case, Casey Christopher

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using

TITLE OF INVENTION: Langer Proteins

FILE REFERENCE: 019496-002200US

CURRENT APPLICANTION NUMBER: US/09/229,037A

NUMBER OF SEQ ID NOS: 40

SEGTWARET PLILIG DATE: 1999-01-12

NUMBER PROS: PatentIN Ver. 2.0
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                                                          FEATURE: OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP OTHER INFORMATION: construct targeting upstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
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US-09-779-233-3
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100.0%; Pred. No. 0.91;
tive 0; Mismatches 0; Indels
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Patent No. 668958
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
LENGTH: 99
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  LENGTH: 99
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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nes 7; Conservative
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US-09-779-233-3
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LENGTH: 196
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APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Brach E.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
TITLE OF INVENTION: USING ZINC 2 US
TITLE OF INVENTION: USING ZINC 2 US
CURRENT APPLICATION NUMBER: US/09/478, 681
CURRENT FILING DATE: 2000-01-06
CURRENT PAPLICATION NOS: 43
SOFTWARE: PATENTIN VOS: 43
LENGTH 196
TYPE. NOT
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100.0%; Score 7; DB 4; Length 196; 100.0%; Pred. No. 1.6;
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100.0%; Pred. No. 1.6;
tive 0; Mismatches
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100.0%; Pred. No. 1.6;
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Sequence 18, Application US/09779233

Patent No. 6689558

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REFERENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 18

LENGTH: 196
                                          0; Mismatches
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; Patent No. 6607882
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ORGANISM: Artificial Sequence
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Best Local Similarity 10v..
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Search completed: December 27, 2004, 18:12:05 Job time : 15.8 secs

Gaps

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Scoring table:

Word size :

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Result Š

Perfect score:

Sequence:

OM protein

Run on:

Length 21;

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APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
TITLE OF INVENTION: to Bind to Preselected Sites
TITLE OF INVENTION: to Bind to Preselected Sites
CURRENT APPLICATION NUMBER: US/10/113,424
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US/09/229,007A
PRIOR PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence; CTHER INFORMATION: (F1, F2, F3) from SBS design GL-8.3.1 US-10-113-424-97
                                                                                                                                                                                                                                                               CTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2, F3) from SBS design GL-8.3.1 US-09-229-007A-97
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100.0%; Pred. No. 0.04;
ive 0; Mismatches
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APPLICANT: Gendaq Limited
TITLE OF INVENTION: Screening System
FILE REFERENCE: 674538-2003
CURRENT APPLICATION NUMBER: US/09/851,271A
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: PCT/GB99/03730
PRIOR FILING DATE: 1999-11-09
CURRENT APPLICATION NUMBER: US/09/229,007A CURRENT FILING DATE: 1999-01-12 NUMBER OF SEQ ID NOS: 97 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 97
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Patent No. 6733970
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Patent No. 6785613
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APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
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15 RSDNLTR 21
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Matches 7; Conser
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Sequence 97, Application US/09229007A
Sequence 97, Application US/09229007A
Sequence 97, Application US/09229007A
SPECICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Applicant, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
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Sequence 2, Appli
Sequence 15, Appl
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                                                                                                                                                                                                                 ; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-113-424-97

US-09-85-1-271A-2

US-09-424-487B-2

US-09-395-448-15

US-09-912-796-15

US-09-941-450-15
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Maximum DB seq length: 2000000000
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Batent No. 6599692

Batent No. 6599692

Batent No. 6599692

APPLICANT: Case, Casey C.

APPLICANT: Zhang, Lei

APPLICANT: Sangamo Biosciences, Inc.

IITLE OF INVENTION: Punctional Genomics Using Zinc Finger Proteins
FILE REFERENCE: 019495-002000US

CURRENT APPLICATION NUMBER: US/09/395,448

CURRENT FILING DATE: 1999-09-14

PRIOR APPLICATION NUMBER: 09/229,007

PRIOR APPLICATION NUMBER: 09/229,037
                                                                                                                                                                       FEATURE:
NAME/KEY: ZN FING
LOCATION: (1)...(88)
OTHER INFORMATION: protein sequence encoding a zinc-finger domain US-09-851-271A-2
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Patent No. 6746838
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: CHOO, YEN
APPLICANT: KLUG, AARON
APPLICANT: ISALAN, MARK
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
FILE REFERENCE: 71278/264975
CURRENT APPLICATION NUMBER: US/09/424,487B
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: GB 9710809.6
PRIOR APPLICATION NUMBER: PCT/GB98/01512
PRIOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
SOUTHARRE: PATENTING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
SEQ ID NO S: 21
LENGTH: 88
PRIOR APPLICATION NUMBER; GB9824544.2
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 88
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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45 RSDNLTR 51
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US-09-424-487B-2
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US-09-395-448-15
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US-09-925-796-15

Sequence 15, Application US/09925796

Patent No. 6777185

GENERAL INFORMATION:

APPLICANT: Chang, Lei

APPLICANT: Sangamo Biosciences, Inc.

FILE REFERENCE: 01946-002000US

CURRENT FILING DATE: 1999-09-14

PRIOR PELING DATE: 1999-09-14

PRIOR PELING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 23

SOGTWARE: Patentin Ver. 2.1

SEQ ID NOS: 23
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US-09-941-450-15
Sequence 15, Application US/09941450
Patent No. 6780590
GENERAL INFORMATION:
APPLICANT: Gase, Casey C.
APPLICANT: Urnov, Fyodor
FILE REFERENCE: S7.US3 / 8325-0007.20
CURRENT APPLICATION NUMBER: US/09/941,450
CURRENT APPLICATION NUMBER: 09/995,448
PRIOR APPLICATION NUMBER: 09/395,448
PRIOR PRILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 15
LENGTH: 97
LENGTH: 97
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-01-1
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 97
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; ORGANISM: Artificial Sequence; ; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:designed ZFP
US-09-941-450-15

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: December 27, 2004, 18:12:05
Job time: 15.8 secs
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Sequence 16192, A
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
   /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-09-248-796A-16192
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; Sequence 42, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
GENERAL TORORMATION:
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
; SOFTWAREN FILING DATE: 2001-02-08
; SOFTWAREN PATENTION VET: 2.0
; SEQ ID NO 42
LENGTH: 7
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                     US-09-846-033B-41
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Maximum DB seq length: 2000000000
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US-09-779-233-42
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Sequence 16192, Application US/09248796A

Sequence 16192, Application US/09248796A

Patent No. 6434137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: 1990-132

CURRENT APPLICATION NUMBER: US/09/248,796A

FILE REFERENCE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16192
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Length 7;
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100.0%; Pred. No. 0.23;
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; ORGANISM: Candida albicans
US-09-248-796A-16192
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Best Local Similarity 100...
Local 7; Conservative
                                      Conservative
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Result Š.

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GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Riug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                     CTHER INFORMATION: Description of Artificial Sequence:SBS7 (OTHER INFORMATION: recognition helix US-09-731-558-18
                                                                                                                                                                                                                           DB 4; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pillabury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 7; 100.0%; Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-UTL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9412634.9
FILING DATE: 08-NOV-1994
FILING DATE: 20-NOV-1994
INPORMATION FOR SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 73, Application US/09139762A
Patent No. 6013453
                                                                                                                                                                                                                                                                       ö
                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
          SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 7
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Best Local Similarity 100.
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MOLECULE TYPE: peptide
NUMBER OF SEQ ID NOS: 24
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Sequence 18, Application US/09731558

Patent No. 650317

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Rangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019496-0032100S

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT PLINIG DATE: 2000-12-06

PRIOR FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    (without alignments)
29.381 Million cell updates/sec
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Sequence 73, R
Sequence 84, R
Sequence 99, R
Sequence 13, R
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                                                                                                                                            December 27, 2004, 17:02:31 ; Search time 15.8 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-139-762A-73
US-09-139-762A-84
US-09-139-762A-99
US-08-793-408-13
US-09-139-762A-13
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Maximum DB seq length: 2000000000
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Query
Match Length DB
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Gape

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Sequence 13, Application US/08793408
| Sequence 13, Application US/08793408
| Patent No. 6007988
| GENERAL INFORMATION:
| APPLICANT: Choo, Yen |
| APPLICANT: Sanchez Garcia, Isidro |
| TITLE OF INVENTION: Improvements in or Relating to |
| TITLE OF INVENTION: Binding Proteins for Recognition of DNA |
| NUMBER OF SEQUENCES: 18 |
| CORRESPONDENCE ADDRESS: |
| STREET: 1100 New York Avenue, N.W. |
| CITY: Washington |
| CITY: Washington |
| STATE: D.C. |
| STATE
Improvements in or Relating to Binding Proteins for Recognition of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 10;
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TITLE OF INVENTION: Improvements in or Relatin TITLE OF INVENTION: Binding Proteins for RecognumBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
STREET: Billebury Madison & Sutro, L.L.P., STREET: H100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 7; DB 3; 100.0%; Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN 1997
PRILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
PRIOR APPLICATION UMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
SPELICATION NUMBER: GB 991680.4
FILING DATE: 20-AUG-1994
SPELICATION NUMBER: GB 991680.4
FILING DATE: 20-AUG-1994
SPELICATION TONE SEQ ID NO: 99: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                 CITY: D.C.
COUNTRY: U.S.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TOWN TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 amino acids
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Best Local Similarity 100...
7; Conservative
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OPERATING SYSTEM:
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                                 WESULT 3
US-09-139-762A-84
is Sequence 84, Application US/09139762A
is Sequence 84, Application US/09139762A
is Patent No. 6013453
is GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Along, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
TITLE OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
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CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/793,408

FILING DATE: 02-JUN-1997

APPLICATION NUMBER: PCT/GB95/01949

FILING DATE: 17-AuG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9514698.1

FILING DATE: 18-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9422534.9

FILING DATE: 08-NOV.1994

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: GB 9416880.4

FILING DATE: 20-AuG-1994

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TENTAMBER: 10 amino acids

TENTAMBER: 10 amino acids

TENTAMBER: 10 amino acids

TENTAMBER: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3918
...
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 99, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 7; Conservative
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US-09-139-762A-99
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Gaps

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 7; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 anino acid
TYPE: anino acid
STRANDEDNESS:
                                                                                                                                                                                       TOPOLOGY: unknown; MOLECULE TYPE: peptide US-09-139-762A-13
                                                                                                                                                                                                                                                                                                                                                                                                                           18 ERGTLAR 24
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Sequence 13, Application US/09139762A

Sequence 13, Application US/09139762A

BALICANT: Choo, Yen

APPLICANT: Choo, Yen

APPLICANT: Choo, Yen

APPLICANT: Sanchez Garcia, Isidro

APPLICANT: Sanchez Garcia, Isidro

TITLE OF INVENTION: Binding Proteins for Recognition of DNA

NUMBER OF ESQUENCES: 125

CORRESPONDENCE ADDERSS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

COUNTRY: Washington

STREET: 1100 New York Avenue, N.W.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READBLE FORM:

WEDIUM TYPE: Diskette

COMPUTER READBLE FORM:

WEDIUM TYPE: USA

SOFTWARE: Word Perfect

COMPUTER: IBW PC compatible

OPERATING SYSTEM: PC-COS/WS-DOS

SOFTWARE: Word Perfect

CHRENT APPLICATION NUMBER: US/09/139,762A

FILING DATE: 02-UN-1997

FILING DATE: 17-AUG-1995

PRICH APPLICATION NUMBER: PCT/GB95/01949

FILING DATE: 17-AUG-1995

PRICH APPLICATION NUMBER: GB 9514698.1

FILING DATE: 18-UUL-1995

PRICH APPLICATION NUMBER: GB 9422534.9

FILING DATE: 18-UUL-1995

PRICH APPLICATION NUMBER: GB 9422534.9
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                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01949
FILLING DATE: 17-AuG-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILLING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILLING DATE: 0-AuG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILLING DATE: 20-AuG-1994
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,408
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 7; Conservative
              Word Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-793-408-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 ERGTLAR 24
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US-09-139-762A-13
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Database :

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Sequence 75, Application US/09139762A

Patent No. 6013453

GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pillabury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: Washington
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillabury Madison & Sutro, L.L.P.
STREST: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
ZIP: 20005-3918
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
FILING DATE: 17-AUG-1995
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA: GB 9422534.9
FILING DATE: 08-904
PRIOR APPLICATION DATA: GB 941680.1
FILING DATE: 08-904
PRIOR APPLICATION DATA: GB 941680.4
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA: GB 941680.4
FILING DATE: 20-AUG-1994
PRIOR APPLICATION DATA: APPLICATION DATA: GB 941680.4
FILING DATE: 20-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 7;
100.0%; Pred. No.
ive 0; Mismatcl
                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
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COUNTRY: USA
ZIF: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketce
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity luv.
Lac 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-139-762A-72
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-09-139-762A-75
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Sequence 113, Appli
Sequence 113, App
Sequence 12, Appl
Sequence 12, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         (without alignments)
29.381 Million cell updates/sec
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Sequence 114,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                               December 27, 2004, 17:02:31 ; Search time 15.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents AA:*
1: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-139-762A-75
US-09-139-762A-93
US-09-424-487B-114
US-09-424-487B-113
US-08-793-408-12
US-08-793-408-12
US-09-424-487B-112
US-09-424-487B-112
US-08-793-408-12
US-08-793-408-12
US-08-793-408-12
US-08-793-408-12
US-08-793-408-18
US-08-139-762A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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    protein search, using sw model

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                                                                                                                                                                                                                                                                         US-09-846-033B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                      1 DRSSLTR 7
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Score

Result

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Gaps

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DB 3; Length 10; 0.15; 0; Indels

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US-09-424-487B-114
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: CHOO, YEN
APPLICANT: CHOO, YEN
APPLICANT: ISALAN, MARK
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
FILE REFERENCE: 71278/264975
CURRENT APPLICATION NUMBER: US/09/424,487B
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: GB 9710809.6
PRIOR FILING DATE: 1997-05-23
PRIOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 114
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: CHOO, YEN
APPLICANT: CHOO, YEN
APPLICANT: SALAM, MARK
ITILE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
FILLE REFERENCE: 71278/264975
CURRENT APPLICATION NUMBER: US/09/424,487B
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: GB 9710809.6
PRIOR PELICATION NUMBER: EP97-05-23
PRIOR PILING DATE: 1997-05-23
PRIOR PILING DATE: 1998-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 7; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-424-487B-114
; Sequence 114, Application US/09424487B
; Patent No. 6746838
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09424487B; Patent No. 6746838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                   APPLICATION NUMBER: GB 94
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 93
                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-93
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US-09-424-487B-9
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APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Sanche Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 10; 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                    PRICA APPLICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION NUMBER: GB 9514698.1
FILING DATE: 19-UUL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
FILING DATE: 20-AUG-1994
FILING DATE: AD-AUG-1994
FILING 
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
PILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
PRIOR APPLICATION NUMBER: GB 9514698.1
PRIOR APPLICATION NUMBER: GB 9714698.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COMPUTE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
COMPUTER: BW PC compatible
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                             APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-139-762A-93
Sequence 93, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRSSLTR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DRSSLTR 7
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COMPUTEY: USA
ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBER: PCT/GB95/01949
17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILLING DATE:
APPLICATION NUMBER: PCT/GB95/01949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-139-762A-12
; Sequence 12, Application US/09139762A
; Patent No. 6013453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                              FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Zinc finger
CTHER INFORMATION: peptide
US-09-424-487B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08793408

Ratent No. 6007988
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 7; DB 4; Length 28; 100.0%; Pred. No. 0.38;
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                                                                                                                                                                                                                     100.0%; Score 7; DB 4; Length 28; 100.0%; Pred. No. 0.38;
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CHOO, YEN
APPLICANT: CHOO, YEN
APPLICANT: ISALAN, MARK
TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
FILE REFERENCE: 71278/264975
CURRENT APPLICATION NUMBER: US/99/424,487B
CURRENT APPLICATION NUMBER: GB 9710809.6
PRIOR APPLICATION NUMBER: PCT/GB98/01512
SROOR FILING DATE: 1998-05-26
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New York Avenue, N.W.
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 28
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-424-487B-113
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US-08-793-408-12
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APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanches Gercia, Isidro
APPLICANT: Sanches Gercia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
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Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels
FILING DATE:
CLASSIFICATION: 435
PRICA PERIOD DATE:
PRICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRICA APPLICATION DATA:
PRICA PERIOD D
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Gaps

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FEATURE:
NAME/KEY: ZN FING
LOCATION: (1)..(88)
OTHER INFORMATION: protein sequence encoding a zinc-finger domain US-09-851-271A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                             DB 4; Length 88, 1.1;
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CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
RECOR APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
FRIOR APPLICATION NUMBER: GB 9412534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
APPLICATION NUMBER: AB 9416880.4
                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,408
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION WHEBE: GB982454.2
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
LENGTH: 88
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; Patent No. 6007988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-AUG-1994
                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Zinc finger; OTHER INFORMATION: peptide
US-09-424-487B-112
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                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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; Batent No. 6746838
; GENERAL INPORMATION:
; GENERAL INPORMATION:
; APPLICANT: CHOO, YEN
APPLICANT: KLUG, AARON
; APPLICANT: ISALAN, MARK
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS
; FILE REFERENCE: 71278/264975
; CURRENT APPLICATION NUMBER: US/09/424,487B
; CURRENT PILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: GB 9710809.6
; PRIOR FILING DATE: 1998-05-23
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 312
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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TITLE OF INVENTION: Screening System
FILE REFERENCE: 674538-2003
CURRENT APPLICATION NUMBER: US/09/851,271A
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: PCT/GB99/03730
  APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09851271A; Patent No. 6733970; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          LENGTH: 33 amino acids IYPE: amino acid
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-09-139-762A-12
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18 DRSSLTR 24
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Best Local Similarity
Matches 7; Conserv
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US-09-139-762A-18

US-09-139-762A-18

PATENT NO. 6013453

GENERAL INPORTION:
APPLICANT: Cho, Yen
APPLICANT: Cho, Yen
APPLICANT: Riug, Aaron
APPLICANT: Riug, Aaron
APPLICANT: Riug, Aaron
APPLICANT: Sanchas Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Instance of the compatible of the comp
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             Pred. No. 1.1;
100.0%; Preα. ν.ς. -
n.ive 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
                Best Local Similarity 100.
Matches 7; Conservative
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18 DRSSLTR 24
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Search completed: December 27, 2004, 18:12:04 Job time : 15.8 secs

DRSSLTR 24

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Appl Appl Appl Appl Appl

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Sequence
Sequence 44,
Sequence 8, Appl.
Sequence 1278, App
Patent No. 5206152
Sequence 6, Appli
Tuence 2, Appli
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                                       Sequence 3
Sequence 3
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Sequence 4
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| Squence 19, Application US/09139762A
| Patent No. 6013453
| GENERAL INFORMATION:
| APPLICANT: Klug, Aaron
| APPLICANT: Klug, Aaron
| APPLICANT: Sanchez Garcia, Isidro
| TITLE OF INVENTION: Improvements in or Relating to
| TITLE OF INVENTION: Binding Proteins for Recognition of DNA
| NUMBER OF SEQUENCES: 125
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
| STREET: 1100 New York Avenue, N.W.
| CITY: Washington
| STATE: D.C.
              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-09-614-679A-19
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US-09-500-700-5
US-08-224-482-11
US-08-863-813A-34
US-08-663-813A-34
US-08-676-118A-34
US-09-500-700-34
US-09-500-700-34
US-09-500-700-44
US-09-500-700-44
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US-09-500-700-44
US-09-500-700-44
US-09-500-700-44
US-09-538-092-1278
US-08-224-482-6
US-08-224-482-6
US-09-538-092-1278
US-08-224-482-6
US-09-538-092-1278
US-09-919-039-66
                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09614679A; Sequence 19, Application US/09614679A; Patent No. 6492117; GENERAL INFORMATION:
APPLICANT: CHOO, YEN
APPLICANT: PALL, SACHIN
APPLICANT: LIU, XIAOHAI
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 71278/271599
CURRENT FILING DATE: 2000-07-12
CURRENT FILING DATE: 2000-07-12
SOUTHARE: PATENTIN VET: 2.1
SEQ ID NO 19
LENGTH: 7
CHOOS: 24
SOUTHARE: PATENTIN VET: 2.1
SEQ ID NO 19
                                                                                                                                                                                                                                                              ALIGNMENTS
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.،
نام 7; Conservative
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US-09-614-679A-19
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    FEATURE:
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Patent No. 5206152
Sequence 1, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 5, Appli
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Sequence 53, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 95, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1, Appl
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29.289 Million cell updates/sec
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Sequence 70,
Sequence 13,
Sequence 7, A
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Sequence 8,
Sequence 8,
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-139-762A-19
US-09-139-762A-19
US-08-040-548-19
US-08-46-344-19
US-09-229-007A-95
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US-10-113-424-95
US-09-058-459-1
US-09-058-459-1
US-09-058-459-1
US-09-127-926-1
US-09-127-926-1
US-09-1240-1798-15
US-09-144-357-1
US-09-240-179-2
US-09-240-179-2
US-09-140-654-7
US-09-140-637-13
US-08-466-344-7
US-08-466-344-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                            2004, 19:21:38
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                               Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
                                                                                                                                                US-09-846-033B-94
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Match Length
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                                                                                                                                                                         1 RSDHLTT 7
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                                                                                                                                                                                                                                                                  7
                                                                                                                                                             Perfect score:
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Word size :

Searched:

Sequence:

Title:

on:

Database :

Result Š. ö

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Gaps
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Patent No. 15763209
GENERAL INFORMATION:
APPLICANT: SUKhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5763209th Clark Street, Suite 800
CITY: Chicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 7; Conservative 0; Mismatches 0; Indels
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COMPUTER: 11linois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F:
REGISTRATION NUMBER: arcd667
TELEFORMINICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMINICATION SEQ ID NO: 19:
SEQUENCE GIARACTERISTICS:
TENERAL COURTERISTICS:
                 FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-ULL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: GB 942534.9
FILING DATE: 20-AUG-1994
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aning acids
UMBER: PCT/GB95/01949
17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 20 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-040-548-19
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US-09-139-762A-53
US-09-139-762A-53
i Sequence 53. Application US/09139762A
j Patent NO. 6013453
i GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Ranchez Garcia, Isidro
ITLE OF INVENTION: Improvements in or Relating to
ITLE OF INVENTION: Improvements in or Relating to
ITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ITPLICATION NEW ENCHOLOGY/MS-DOS
SOFTWARE: BMP PC compatible
COMPUTER: BMP PC compatible
COMPUTER: Word Perfect
CURRENT APPLICATION NUMBER: US/09/139,762A
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                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UN-1997
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-UL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
          ZOUTO TO THE TOTAL TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSDHLTT 7
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FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTHARE: Patentin Ver. 2.1
SEQ ID NO 95
LENGTH: 21
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ORGANISM: Artificial Sequence
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
---- 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-113-424-95
                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                FEATURE:
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Sequence 95. Application US/09229007A
Patent No. 6453242
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: ApplicANT: Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger
TITLE OF INVENTION: to Bind to Preselected Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SUNDARME, VIKAB P.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE

TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSE: Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: COUGHLIN, Daniel F.
REGISTRATION NUMBER: 36,111
REFRENCE/CONTIN INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          3: Arnold, White & Durkee
321 No. 5773583th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        US-08-466-344-19; Sequence 19, Application US/08466344; Patent No. 5773583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECURION: (312) /**
TELEPAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
'FWGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||||
9 RSDHLTT 15
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CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
                                                                                RSDHLTT 15
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                                     RSDHLTT 7
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US-08-466-344-19
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Sequence 95. Application US/10113424

| Sequence 95. Application US/10113424
| Patent No. 6785613
| CENERAL INFORMATION:
| APPLICANT: Elsenberg, Stephen P. |
| APPLICANT: Estat. Edward J. |
| APPLICANT: Case, Casey C. |
| APPLICANT: Sangamo Biosciences, Inc. |
| APPLICANT: Sangamo Biosciences, Inc. |
| APPLICANT: Sangamo Biosciences, Inc. |
| APPLICANT: Sept. Edward J. |
| FILE OF INVENTION: Proceeding and Methods of Designing Zinc Finger Proteins |
| FILE REFERENCE: 019496-001800US |
| CURRENT APPLICATION NUMBER: US/09/229,007A |
| PRIOR FILING DATE: 1999-01-12 |
| NUMBER OF SEQ ID NOS: 97 |
| SEQ ID NO 95 |
| LENGTH: 21 |
| LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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US-10-113-424-95
CTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-09-229-007A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Patent No. 5928955
GENERAL INFORMATION:
APPLICANT: Imperiali, Barbara
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                Length 21;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08466344

Patent No. 5773583

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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100.0%; Score 7; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
SIREL:
SOFTWARE:
SOFTING DATA:
APPLICATION NUMBER:
SOFTWARE:
SOFTWAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100،۰
ابر 7; Conservative
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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MOLECULE TYPE: peptide
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                                                                                                      TYPE: amino actributes: sing
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9 RSDHLTT 15
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US-08-466-344-34
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US-09-058-459-1
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| Sequence 34, Application US/08040548
| Sequence 34, Application US/08040548
| Patent No. 5763209
| Patent No. 5763209
| Patent No. 5763209
| TITLE OF INVENTION: WETHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: WETHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: WORTHODS AND MATERIALS OF SEQUENCES: 67
| CORRESPONDENCE ADDRESS: 67
| ADDRESSEE: Arnold, White & Durkee STREET: 321 No. 5763209th Clark Street, Suite 800
| CTIT: Chicago | STATE: Illinois
| COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                 STREET: NECTOWER - SUICE 3500, 455 N. CLEVILOIDE
STREET: Plaza Drive
CITY: Chicago
STATE: 111inois
COMPUTE: 111inois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN Release #1.0, Version #1.30
SURTARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION NUMBER: US/08/620,151
FLING DATE: 22-MAR-1996
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen L.
REPERBENCE/DOCKET NUMBER: 8597/6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TENERAL AND TELECOMMUNICATION:
TELECOMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELE
    ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36.111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: peptide
US-08-620-151-111
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US-09-037-179B-15
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Sequence 1, Application US/09127926

Sequence 1, Application US/09127926

GENERAL INFORMATION:

APPLICANT: Baliyat, Bassil L.

APPLICANT: Street, Arthur

APPLICANT: Su, Yacying

TITLE OF INVENTION: Apparatus and Method for Automated Protein Design

FILE REFREENCE: A55353-4/FFT/RMS/SJR

CURRENT APPLICATION NUMBER: US/09/127,926

CURRENT FILING DATE: 1999-07-31

PRIOR PILING DATE: 1997-04-11

PRIOR FILING DATE: 1997-04-11

PRIOR FILING DATE: 1997-06-04

PRIOR FILING DATE: 1997-10-03

PRIOR APPLICATION NUMBER: 60/061,097

PRIOR APPLICATION NUMBER: 60/061,097

PRIOR APPLICATION NUMBER: 60/087,561

PRIOR PILING DATE: 1998-04-10

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1998-06-01
                                                               APPLICANT: Mayo, Stephen L.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Gordon, D. B.
APPLICANT: Gordon, D. B.
TITLE OF INVENTION: APPRATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
FILE REFERENCE: Action NUMBER: US/09/058,459
CURRENT FILING DATE: 1097-04-10
PRIOR APPLICATION NUMBER: 60/043,464
PRIOR APPLICATION NUMBER: 60/043,464
PRIOR PLLING DATE: 1997-04-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 7; DB 3; Length 28; 100.0%; Pred. No. 0.043; ive 0; Mismatches 0; Indels
Sequence 1, Application US/09058459
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Best Local Similarity 100..
7, Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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SOFTWARE: Patentin VA
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSDHLTT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-127-926-1
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14 RSDHLTT 20

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FACEUL NO. 03.10.480

FACEUL NO. 03.10.480

FACEUL NO. 03.10.480

APPLICANT: Greisman, Harvey A.

APPLICANT: Greisman, Harvey A.

APPLICANT: Greisman, Harvey A.

APPLICANT: Massachusetts Institute of Technology

TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc

TITLE OF INVENTION: A Finger Proteins for Diverse DNA Target Sites

TITLE REFERENCE: 013496-0002005

TITLE REFERENCE: 013496-002005

CURRENT APPLICATION NUMBER: US 60/073,223

EARLIER APPLICATION NUMBER: US 60/073,223

EARLIER PILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 65

SEQ ID NO 2

LENGTH: 28
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US-09-240-179-2
                                                                                                                                                                                                        APPLICANT: Pelletier, Jerry, APPLICANT: Pelletier, Jerry, APPLICANT: Pelletier, Jerry, APPLICANT: Pelletier, Jerry, APPLICANT: Haber, Daniel A. APPLICANT: Housman, David B. APPLICANT: Bruening, Wendy, APPLICANT: Bruening, Wendy, APPLICANT: Daviel, Andre TITLE OF INVENTION: Localization and Characterization of the TITLE OF INVENTION: Wilms' Tumor Gene TITLE OF INVENTION: WWHER: US/09/037,179B CURRENT APPLICATION WUMBER: US/09/037,179B CURRENT FILING DATE: 1998-03-09 PRIOR FILING DATE: 1993-08-02 PRIOR FILING DATE: 1993-08-02 PRIOR PAPLICATION NUMBER: US 07/614,161 PRIOR APPLICATION NUMBER: US 07/435,780 PRIOR FILING DATE: 1999-11-13 PRIOR FILING DATE: 1999-11-13 PRIOR FILING DATE: 1999-11-13 PRIOR FILING DATE: 1994-09-27 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 7; DB 3; Length 28; 100.0%; Pred. No. 0.043; ive 0; Mismatches 0; Indels
5, Application US/09037179B
6316599
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Patent No. 6410248
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                                                                                            APPLICANT: Call, Katherine M. APPLICANT: Glaser, Thomas M. APPLICANT: Ito, Caryn Y. APPLICANT: Buckler, Alan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
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ORGANISM: Homo sapien
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17 RSDHLTT 23
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Query Match 100.0%; Score 7; DB 4; Length 28; Best Local Similarity 100.0%; Pred. No. 0.043; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Search completed: December 27, 2004, 20:31:04 Job time: 15.85 secs
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13 RSDHLTT 19
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14 RSDHLTT 20
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

December 27, 2004, 19:21:38 ; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec

US-09-846-033B-93 7 1 RSDNLTQ 7 Title: Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

478139 segs, 66318000 residues Searched:

7 Word Bize :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

lssued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

H Query Score Match Length DB . 02

No matches found

Search completed: December 27, 2004, 20:31:04 Job time : 15.85 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 27, 2004, 19:21:38 ; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec

US-09-846-033B-92 1 QRAHLAR 7 Title: Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

478139 segs, 66318000 residues Searched:

Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2 6/ptodata/l/iaa/5A COMB.pep:*
2: /cgn2 6/ptodata/l/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/l/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/l/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/l/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/l/iaa/PCTUS COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB

No matches found

Search completed: December 27, 2004, 20:31:04 Job time : 15.85 secs

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Scoring table:

Word size :

Database

Searched:

Perfect score:

Run on:

Sequence:

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OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix
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100.0%; Pred. No. 3.8e+05;
iive 0; Mismatches 0;
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Fatent No. 668958
GENERAL INFORMATION:
APPLICANT Case, Casey
TITLE OF INVENTION:
FILE REPERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT APPLICATION NUMBER: US/09/779,233
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
PRIOR APPLICATION NUMBER: US 09/456,100 PRIOR FILING DATE: 1999-12-06 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity
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1 RSDHLSR 7
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                                                                                                                                            TYPE: PRT
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Patent No. 650371.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REPERENCE: 019496-00321008
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
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Sequence 15,
Sequence 15,
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-44
US-09-229-037-15
US-09-779-233-3
US-09-779-233-3
US-09-779-233-18
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Maximum DB seq length: 2000000000
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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81 RSDHLSR 87
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APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey, Casey Christopher
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sisenberg, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Singamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using TITLE OF INVENTION: Zinc Finger Proteins
FILE REPERENCE: 019496-0022000S
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
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US-09-478-681-15

Sequence 15, Application US/09478681

Patent No. 6607882

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Estonberg, Stephen P.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REQUIATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZING FINGER PROTEINS
TITLE OF INVENTION: USING ZING FINGER PROTEINS
FILE REPERENCE: 8325-0002.10 / $2-US3
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43

SOOTWARE: PatentIn Ver. 2.0
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
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                                                                                     100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indels
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US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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LENGTH: 99
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LENGTH: 99
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US-09-229-037-30

Sequence 30, Application US/09229037A

Sequence 30, Application US/09229037A

Sequence 30, Application US/09229037A

Sequence 30, Application US/09229037A

APPLICANT: Case, Casey Christopher

APPLICANT: Case, Casey Christopher

APPLICANT: Spards, Stephen P.

APPLICANT: Spards, Stephen P.

APPLICANT: Spards Biosciences, Inc.

TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using

TITLE OF INVENTION: 2nc Finger Proteins

TITLE OF INVENTION: 2nc Finger Proteins

FILE REFERENCE: 019456-00220001

FULE PRILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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US-09-229-037-30
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                                                                                                        Length 99;
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0.16;
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; Sequence 3, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TTLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; TTLE OF INVENTION: CELLS
; CURRENT APPLICANTON NUMBER: US/09/779, 233
; CURRENT PILING DATE: 2011-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
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                            RESULT 8

US-09-478-681-30

i Sequence 30, Application US/09478681

i Patent No. 6607882

j GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Bracon K.

TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZINC FINGER PROTEINS

TITLE OF INVENTION UNMBER: US/09/478,681

CURRENT FILING DATE: 2000-01-06

SEQ ID NOS: 43

SOFTWARE: PATENTIN Ver. 2.0

LENGTH: 196

LENGTH: 196

LENGTH: 196

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE:

OTHER PINFOLLERS
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; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 668958
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT FALLING DATE: 201-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
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178 RSDHLSR 184
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178 RSDHLSR 184
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US-09-779-233-18
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RESULT 2
US-09-779-233-43
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LENGTH: 7
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Fatent No. 650377

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Liu, Qiang

APPLICANT: Edward J.

APPLICANT: Rebar, Edward J.

APPLICANT: Rebar, Edward J.

TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019496-003210US

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT FILING DATE: 2000-12-06

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 24

SEQ ID NOS: 24

SEQ ID NO 13

LENGTH: 7
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Sequence 43, Appl
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                                                                                                                                 December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-43
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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US-09-779-233-43
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                                                          OTHER INFORMATION: Description of Artificial Sequence:SBS2 OTHER INFORMATION: recognition helix
                                                                                                                                             Query Match 100.0%; Score 7; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 7; DB 4; Length 7; ilarity 100.0%; Pred. No. 3.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 27, 2004, 20:31:03 Job time : 15.85 secs
                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 43, Application US/09779233; Patent No. 6689558; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
7; Conserva
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APPLICANT: CHOO, Yen
APPLICANT: CHOO, Yen
APPLICANT: ULLMAN, Christopher G.
TITLE OF INVENTION: GENE SWITCHES
FILE REFERENCE: 8325-2003 / G7-US1
CURRENT APPLICATION NUMBER: US/09/995, 973
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.0
                                     Sequence 37, Application US/09995973; Patent No. 6706470; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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RSDHLSK 7
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US-09-229-007A-96
                          JS-09-995-973-37
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                                                                                                                                                                                                      SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                   December 27, 2004, 19:21:38 ; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
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Sequence 15,
Sequence 15,
Sequence 15,
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Sequence 7,
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Sequence 96
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Sequence 1
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Sequence 3
Sequence 1
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2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-229-007A-96
US-08-620-151-3
US-08-570-227A-5
US-08-570-227A-6
US-09-077-991-8
US-09-077-991-8
US-09-077-991-9
US-09-077-991-8
US-09-077-991-8
US-09-077-991-8
US-09-077-991-8
US-09-229-007A-9
US-09-229-007A-9
US-09-395-448-15
US-09-395-796-15
US-09-395-796-15
US-09-395-796-15
US-09-229-007A-10
US-09-229-007A-10
US-09-229-007A-10
US-09-239-476-73
US-08-353-476-73
US-08-353-476-116
US-08-353-476-116
US-08-353-476-116
US-08-353-476-116
US-09-538-092-1254
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                               US-09-846-033B-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
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                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                    Word size :
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Database :

Result

Sequence:

е 6

Searched:

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Cox III, George N.
APPLICANT: Sangamo Blosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: Lo Bind to Preselected Sites
FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 96
LEAGTH: 21
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OTHER INFORMATION: Description of Artificial Sequence: zinc finger OTHER INFORMATION: binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2, F3) from SP1
US-09-229-007A-96
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                                                                                                         100.0%; Score 7; DB 4; Length 12; 100.0%; Pred. No. 0.039; ive 0; Mismatches 0; Indele
                                                                                                                                                                    0; Mismatches
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US-10-113-424-96
; Sequence 96, Application US/10113424
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ALIGNMENTS

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Gaps
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Patent No. 5981217
GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T. C.
TITLE OF INVENTION: DNA ENCONDING TGF-BETA INDUCIBLE
TITLE OF INVENTION: EARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED
TITLE OF INVENTION: BARD SPECIAL (TIEF-1), A CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                        Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                     Query Match 100.0%; Score 7; DB 2; Length 26; Best Local Similarity 100.0%; Pred. No. 0.076; Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.19;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FERSERO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,227A
FILING DATE: 11-DEC-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WOESSINEY, WATERN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150.157US1
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REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELERPHONE: 612-359-3263
TELEFAX: 612-359-3263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.º
---nes 7; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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STRANDEDNESS: 817
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TYPE: amino acid STRANDEDNESS:
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US-08-570-227A-5
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US-08-570-227A-6
                                                             ; TOPOLOGY:
; MOLECULE TY
US-08-620-151-3
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                        APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Case Casey C.
APPLICANT: Rebar, Edward J.
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biscience, Inc.
APPLICANT: Saloacion of Sites for Targeting by Zinc Finger
ITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
ITLE OF INVENTION: Proteins and Methods of Sites
ITLE OF INVENTION: Proteins and Methods of Sites
ITLE OF INVENTION: Designing Zinc Finger Proteins
ITLE OF INVENTION: US BIND CASE CONSENT APPLICATION NUMBER: US/10/113,424
CURRENT APPLICATION NUMBER: US/09/229,007A
PRIOR APPLICATION NUMBER: US/09/229,007A
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 96
IENGTH: 21
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US-10-113-424-96
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GENERAL INFORMATION:

APPLICANT: Malkup, Grant K.

TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR TITLE OF INVENTION: DIVALENT ZINC

TITLE OF INVENTION: DIVALENT ZINC

NUMBER OF SEQUENCES: 136

CORRESPONDENCE ADDRESS:

ADDRESSE: BRINKS, HOFER, GILSON & LIONE

STREET: ROT Ower - Suite 3600, 455 N. Cityfront

STREET: Plaza Drive

CITY: Chicago

STREET: Plaza Drive

CITY: Chicago

STREET: Plaza Drive

COUNTRY: USA

ZIP: 60611-5599

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION: 422

ATTORNEY/AGENT INFORMATION:

NAME: Shannon, Karen L.

REGISTRATION NUMBER: 36,675

REFERENCE/DOCKET NUMBER: 8597/6

TELECOMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 7; DB 4; Length 21; Best Local Similarity 100.0%; Pred. No. 0.063; Matches 7; Conservative 0; Mismatches 0; Indels
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; Sequence 3, Application US/08620151
; Patent No. 5928955
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
1.RNGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Gaps
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Sequence 7, Application US/09077991

Sequence 7, Application US/09077991

GENERAL INFORMATION:

APPLICANT: Subtamensiam, M.

APPLICANT: Spelsberg, T.C.

APPLICANT: Spelsberg, T.C.

APPLICANT: Roche, P.C.

TITLE OF INVENTION: TIEF-1) and a method to detect breast cancer;

FILE REFERENCE: 150.157052

CURRENT APPLICATION NUMBER: US/09/077, 991

CURRENT FILING DATE: 1996-12-11

EARLIER FILING DATE: 1996-12-11

EARLIER FILING DATE: 1996-12-11

SOFTWARE: PERSECTION NUMBER: US 08/570, 227

EARLIER FILING DATE: 1995-12-11

NUMBER OF SEQ ID NOS: 133

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 7
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100.0%; Score 7; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 7; DB 2; Length 77; 100.0%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
        COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEM VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,227A
FILING DATE: 11-DEC-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT IRFORMATION:
NAME: WOESBNEY, WAITEN D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 150.157US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 10v..
                                                                                                                                                                                                                                                                                                                                                     77 amino acids
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
Diskette
                                                                                                                                                                                                                                                                                  TELEFAX: 612-359-3263
                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-991-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 RSDHLSK 76
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 RSDHLSK 76
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MEDIUM TYPE:
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US-09-077-991-8
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      Sequence 7, Application US/08570227A;
Sequence 7, Application US/08570227A;
Patent No. 5931217;
GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T. C.
TITLE OF INVENTION: DARLY FACTOR-1 (TIEF-1), A GENE EXPRESSED;
TITLE OF INVENTION: BY OSTEOBLASTS;
TITLE OF INVENTION: BY OSTEOBLASTS;
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. BOX 2938
CITY: Minneapolis
STRTE: Minneapolis
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100.0%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches
   Sequence 6, Application US/08570227A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: Tinear; MOLECULE TYPE: peptide US-08-570-227A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 55402
COMPUTER READABLE FORM:
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RESULT 13
US-09-716-637-16
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Sequence 9, Application US/09077991

Sequence 9, Application US/09077991

GENERAL INFORMATION:

APPLICANT: Subramaniam, M.

APPLICANT: Spelsberg, T.C.

APPLICANT: Spelsberg, T.C.

TITLE OF INVENTION: TGF-Beta inducible early factor-1

TITLE REFERENCE: 150.157US2

CURRENT APPLICATION NUMBER: US/09/077,991

CURRENT FILING DATE: 1996-12-11

EARLIER FILING DATE: 1996-12-11

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASELE FASELE PASELE 1999-12-11

SEQ ID NO 9

LENGTH: 77
Sequence 8, Application US/09077991
Fatent No. 6207375
GENERAL INFORMATION:
APPLICANT: Subramaniam, M.
APPLICANT: Spelsberg, T.C.
TITLE OF INVENTION: TGF-Beta inducible early factor-1
FILE REFERENCE: 150.1570S2
FILE REFERENCE: 150.1570S2
FALLIER APPLICATION NUMBER: PCT/US96/19555
EARLIER FILING DATE: 1996-12-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 77
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0.19;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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US-09-077-991-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-077-991-9
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70 RSDHLSK 76
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APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Sandano Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:amino acids OTHER INFORMATION: 531-624 in Sp-1 transcription factor
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100.0%; Pred. No. 0.23;
tive 0; Mismatches
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100.0%; Pred. No. 0.23;
ative 0; Mismatches
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
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Best Local Similarity
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RSDHLSK 84
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Fatent No. 659562

GENERAL INFORMATION:

APPLICANT: Case, Casey C.

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

TILLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins

FILE REFRENCE: 019496-00200003

CURRENT APPLICATION NUMBER: US/09/395,448

CURRENT APPLICATION NUMBER: US/09/395,448

FILE REPERENCE: 1999-01-12

PRIOR APPLICATION UNMBER: 09/229,007

PRIOR FILING DATE: 1999-01-12

NUMBER OF FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 23

SOSTWARE PREDICATION VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence: Sp-1 protein; OTHER INFORMATION: portion US-09-716-637-16
         APPLICANT: EISENBERG, Stephen P.
APPLICANT: EISENBERG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: REBAR, Edward
TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DAFE: 2001-10-12
SOFTWARE: PATENTIN VOS: 35
SOFTWARE: PATENTIN VOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:designed ZFP US-09-395-448-15
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100.0%; Score 7; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 6777185
GENERAL INFORMATION:
APPLICANT: Case, Casey C.
APPLICANT: Zhang, Lei
APPLICANT: Sangamo Biosciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                        SEQ ID NO 16
LENGTH: 94
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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78 RSDHLSK 84
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GENERAL INFORMATION:
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US-09-925-796-15
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US-09-395-448-15
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LENGTH: 97
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rITLE OF INVENTION: Functional Genomics Using Zinc Finger Proteins; FILE REFERENCE: 019496-002000US; CURRENT PEPLICATION NUMBER: US/09/925,796

CURRENT FILING DATE: 2001-08-09

PRIOR FILING DATE: 1999-09-14

PRIOR FILING DATE: 1999-09-14

PRIOR FILING DATE: 1999-09-14

PRIOR FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 97

TYPE: PRT

OTHER INFORMATION: Description of Artificial Sequence: designed ZPP

OUCHY MATCH

US-09-925-796-15

Query Match

Dest Local Similarity 100.0%; Score 7; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 0.24;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

OY 1 RSDHLSK 85

Search completed: December 27, 2004, 20:31:03
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec Run on:

US-09-846-033B-88 Title: Perfect score: Sequence:

1 RSDALTQ 7

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

478139 segs, 66318000 residues Searched:

7 Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database

1soued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description H Query Score Match Length DB Result No.

No matches found

Search completed: December 27, 2004, 20:31:03 Job time : 15.85 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec Run on:

US-09-846-033B-87

1 QSSHLAR 7 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

478139 segs, 66318000 residues

Searched:

1 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database

1seued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

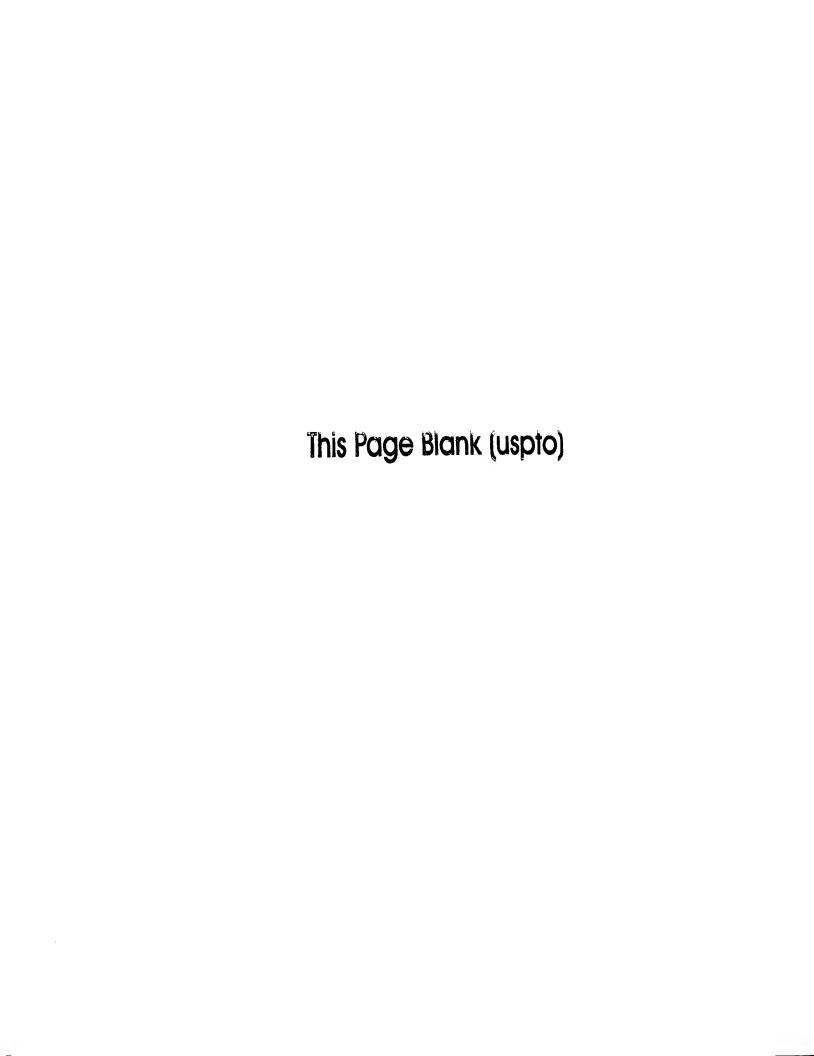
SUMMARIES

C Query Score Match Length DB Result No.

Description

No matches found

Search completed: December 27, 2004, 20:31:03 Job time : 15.85 secs



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                                                                                                                                                                                                                                                               December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-846-033B-86
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Maximum DB seq length: 200000000
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Score Match Length DB
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LENGTH: 7
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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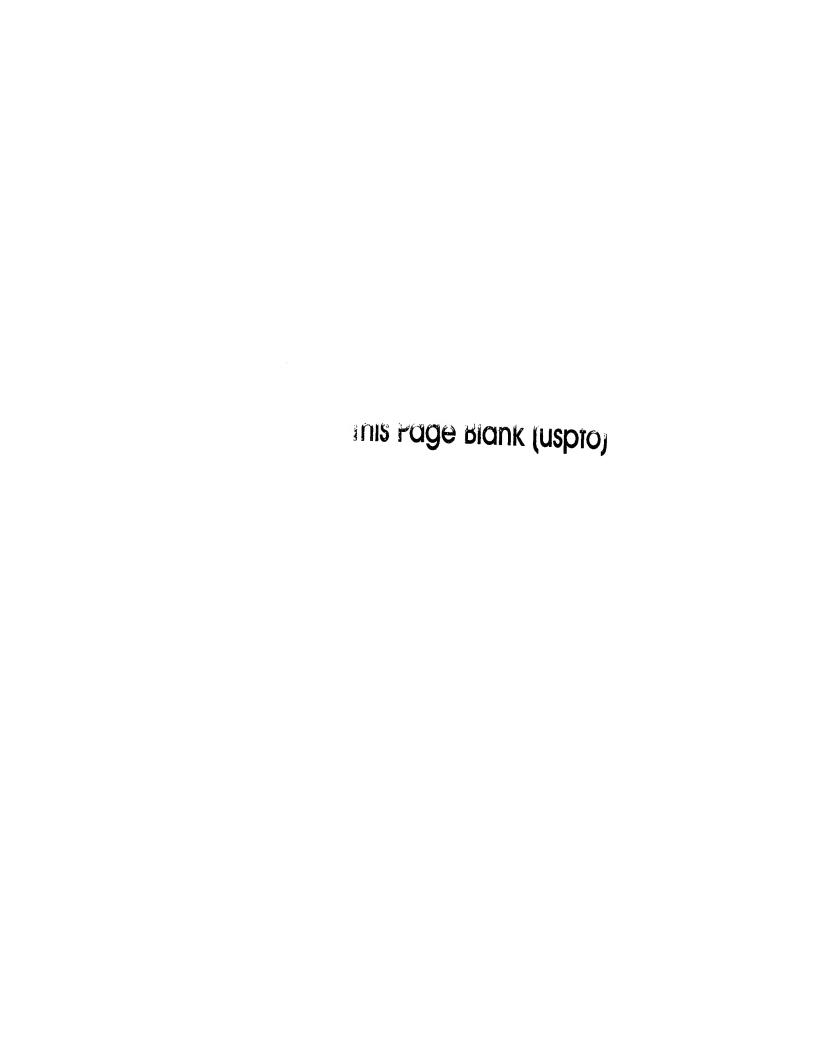
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; ORGANISM: Artificial Sequence; PRAINTER:
; FRATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SBS12;
; OTHER INFORMATION: recognition helix
US-09-731-558-23

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 QSGHLQR 7

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Db 1 QSGHLQR 7

Search completed: December 27, 2004, 20:31:03
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 27, 2004, 19:21:38 ; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec Run on:

US-09-846-033B-84

OLIGO Gapop 60.0 , Gapext 60.0 1 MSHHLSR 7 Title: Perfect score: Sequence: Scoring table:

478139 segs, 66318000 residues Searched:

7 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Issued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

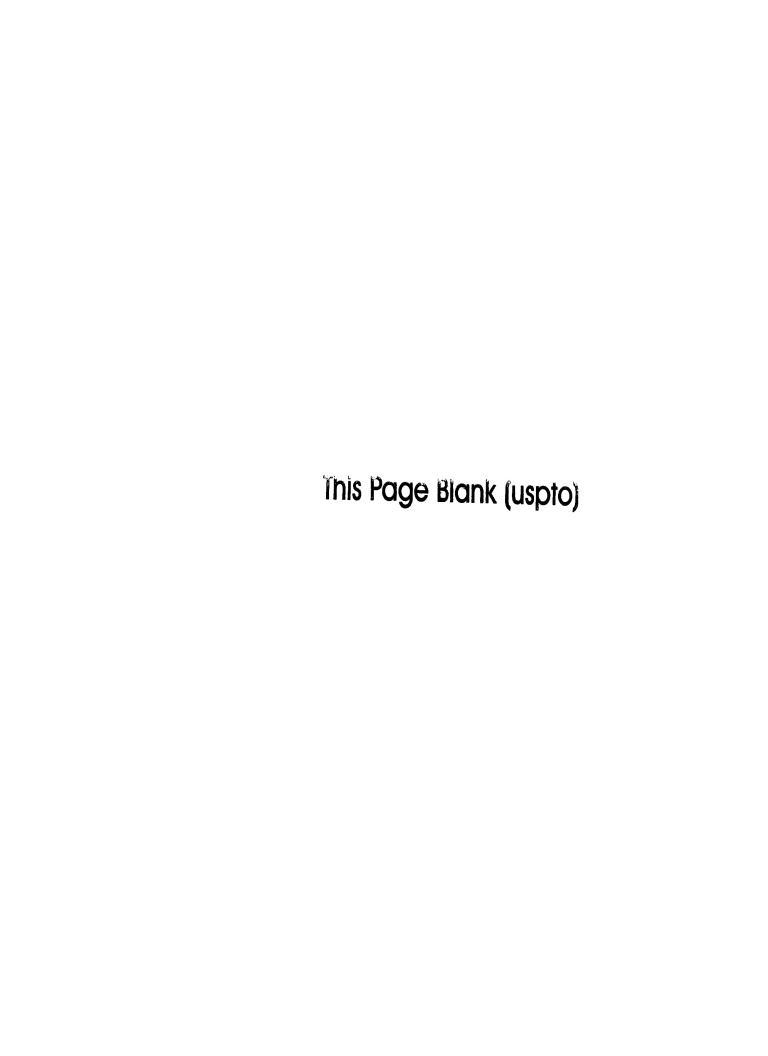
SUMMARIES

G Query Score Match Length DB Result No.

Description

No matches found

Search completed: December 27, 2004, 20:31:02 Job time : 15.85 secs



Gaps

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Indels Length 7;

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Word size :

Searched:

Database :

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APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Canieson, Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Repart J.
APPLICANTON: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Detains and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
CURENT APPLICATION NUMBER: US/09/229,007A
CURENT AILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:phage display; OTHER INFORMATION: selected and mutagenized
US-09-494-190-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223 US-09-229-007A-94
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-494-190-69
iS-09-494-190-69
iS-09-494-190-69
iSequence 69, Application US/09494190
igenerate No. 6610512
igenerate Reference: TSRI 645.2
igenerate APPLICATION NUMBER: US/09/494,190
igenerate Number: 1999-10-14
igenerate Number: 1999-10-14
igenerate Number: 1999-10-14
igenerate Number: 1999-10-16
igenerate Number: 1999-10-16
igenerate Number: US/09/173,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; ive 0; Mismatches 0; Indels
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                                                                                               100.0%; Score 7; DB 3; Le
100.0%; Pred. No. 3.8e+05;
iive 0; Mismatches 0;
, OTHER INFORMATION: codon binding sequence US-09-173-941-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Eisenberg, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                              Query Match
Best Local Similarity 100..
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Matches 7
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LENGTH: 21
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                                                                                                                                                                                                                                  December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
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Sequence 69, 1
Sequence 94, 1
Sequence 94, 1
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Patent No. 6140081

GRNERAL INFORMATION:
APPLICANT: BARBAS, Carlos F.
TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN FILE REFERENCE: NOV0081S
CURRENT APPLICATION NUMBER: US/09/173,941

CURRENT FILING DATE: 1998-10-16

NUMBER OF SEQ ID NOS: 120

SOFTWARE: Patentin Ver. 2.1
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-494-190-69
US-09-229-007A-94
US-10-113-424-94
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                                                                                                                                                                             - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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US-09-173-941-69

SEQ ID NO 69

Score

Result

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Gaps

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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Eleenberg, Stephen P.

APPLICANT: Cox III, George N.

APPLICANT: Application defences, Inc.

TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger Proteins of TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins FILE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins FILE OF INVENTION: Lo Bind to Preselected Sites

TITLE OF INVENTION: Lo Bind to Preselected Sites

FILE REFERENCE: 019496-001800US

CURRENT APPLICATION NUMBER: US/09/229,007A

PRIOR FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 97

SEQ ID NO 94

LENGRIP 21

LENGRIP 21

LENGRIP 21

LENGRIP 22
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                                                    Gaps
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OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence:
CTHER INFORMATION: (F1, F2 and F3) from SBS design GR-223
US-10-113-424-94
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Query Match
100.0%; Score 7; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                 |||||||
8 RSDHLTR 14
                                                                                              1 RSDHLTR 7
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US-10-113-424-94
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Search completed: December 27, 2004, 20:31:02 Job time : 15.85 secs

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1278, Ap 1278, Ap 5206152 6, Appli 2, Appli 2, Appli 6, Appli

Sequence 66,

Sequence

Sequence 44, Sequence 8, 7 Sequence 1278 Patent No. 520 Sequence 6, 7 Sequence 2, 7

Appl Appl Appl Appl Appl Appl Appl

Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 3

Sequence

Run on:

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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-09-614-679A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09139762A; Sequence 19, Application US/09139762A; Patent No. 6013453; GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA; NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 7; DB 4; Length
100.0%; Pred. No. 3.8e+05;
.ive 0; Mismatches 0; Inde
US-09-500-700-5
US-08-224-482-11
US-08-863-813A-34
US-08-863-813A-34
US-08-676-118A-34
US-08-676-118A-34
US-09-500-700-34
US-09-500-700-34
US-09-500-700-44
US-08-676-118A-44
US-08-676-118A-44
US-08-500-700-44
US-08-500-700-44
US-09-538-092-1278
US-08-224-482-8
US-08-224-482-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LIU, XIAOHAI
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 71278/271599
CURRENT APPLICATION NUMBER: US/09/614,679A
CURRENT FILING DATE: 2000-07-12
SUMUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHOO, YEN
APPLICANT: ISALAN, MARK
APPLICANT: PATEL, SACHIN
APPLICANT: BALASUBRAMANIAN, SHANKAR
APPLICANT: LIU, XIAOHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 19, Application US/09614679A
; Patent No. 6492117
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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1 RSDHLTT 7
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LENGTH: 7
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Sequence 1, Appli
Sequence 8, Appli
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                                                                                                                                                                                     December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, A Sequence 1, A Sequence 70, Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-614-679A-19
US-09-139-762A-19
US-09-139-762A-19
US-08-040-548-19
US-09-29-0074-95
US-09-29-0074-95
US-0113-424-95
US-08-040-548-19
US-08-058-459-11
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US-09-124-134
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US-09-716-637-13
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US-08-466-344-7
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US-08-66-344-8
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US-08-66-344-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                        US-09-846-033B-81
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Match Length DB
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                                                                                                                                                                                                                                                                                                                        Perfect score:
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Sequence 19, Application US/08040548

Patent No. 5763209

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67

CORRESPONDENCES: 67

CORRESPONDENCES: Annold, White & Durkee

STREET: 321 No. 5763209th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 7; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 3; Length 10; 100.0%; Pred. No. 0.017; tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA: 48
PRIOR APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: GB 942680.4
FILING DATE: 20-AUG-1994
INFORMATION POR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COUGHLID, Daniel F.
REGISTRATION NUMBER: 36,111
REFREENCE/POCKET NUMBER: arcd
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: peptide
US-08-040-548-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown; MOLECULE TYPE: peptide US-09-139-762A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-08-040-548-19
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US-09-139-762A-53
US-09-139-762A-53
i Sequence 5.3 Application US/09139762A
j Patent No. 6013453
j GENERAL INFORMATION:
i APPLICANT: Choo, Yen
j APPLICANT: Sanchez Garcia, Isidro
i TITLE OF INVENTION: Improvements in or Relating to
j TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES.
i ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET 1100 New York Avenue, N.W.
CITY: Mashington
STATE: D.C.
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               COUNTRY: USA
ZIP: 20005-3918
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: US 08/793,408
FILING DATE: 17-AUG-1995
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 19-JUL-1995
PRIOR APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: GB 942680.4
FILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: GB 9416880.4
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ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 7; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSDHLTT 7
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Length 10;

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Length 21;

us-09-846-033b-81.olig7.rai

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APPLICANT: Eisenberg, Stephen P.
APPLICANT: Case, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Caneson Andrew
APPLICANT: Jamieson, Andrew
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence; CTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-10-113-424-95
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-09-229-007A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 111, Application US/08620151
Patent No. 5928955
GENERAL INFORMATION:
APPLICANT: Imperiall, Barbara
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL PLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 7; DB 4; Length 21; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 7; Conservative 0; Mismatches 0
FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 95
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-113-424-95
; Sequence 95, Application US/10113424
; Patent No. 6785613
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
LENGTH: 21
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                               FEATURE:
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US-09-229-007A-95

Sequence 95, Application US/09229007A

Patent No. 645342

GENERAL INFORMATION:

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Case, Case, Case, C.

APPLICANT: Gase, Case, C.

APPLICANT: Cox III, George N.

APPLICANT: Rebar, Edward J.

TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger

TITLE OF INVENTION: to Bind to Preselected Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                 Sequence 19, Application US/08466344

Batent No. 5773583

GENERAL INFORMATION:
APPLICANT: SUKhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: Day disk

COMPUTER: Day Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,344

FILING DATE: 06-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: 08/040,548

FILING DATE: 31.4MRR.1993

ATTORNEY/AGENT INFORMATION:

NAME: COUGHIN, Daniel F.

REFERENCE/DOCKET NUMBER: arcd067

TELEFONMINICATION INFORMATION:

TELEFONMINICATION INFORMATION:

TELEFONMINICATION INFORMATION:

TELEFONMINICATION OF SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 amino acids
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 321 No. 5
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||||
9 RSDHLTT 15
                                                                                              RSDHLTT 15
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSDHLTT 7
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US-08-466-344-34

j Sequence 34, Application US/08466344

j Requence 34, Application US/08466344

j Ratent No. 5773583

GENERAL INFORMATION:

APPLICANT: Sukhatme, Vikas P.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE

TITLE OF INVENTION: White & DURKEE

CORRESPONDENCE ADDRESS:

ADDRESSES: Arnold, White & Durkee

STREET: 321 No. 5773583th Clark Street, Suite 800

CITY: Chicago

STATE: Illinois

COMPUTE: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTE: READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTE: Plan PC comparible

OPERATING SYSTEM: US/08/466,344

FILING DATE: 06-10N-1995

CLASSIFICATION NUMBER: US/08/466,344

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/101-18

RESERENCE/DOCKET NUMBER: 36,111

RESERENCE/DOCKET NUMBER: 31,000

TELLERAX: (312) 245-4961

INFORMATION POR SED ID NO: 34: SEQUENCE CHARACTERISTICS:

LENGTH: 24,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 1; Length 28; 100.0%; Pred. No. 0.043; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100...
7, Conservative
                          SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: Bir
                                                                                                                                                                                                                                                                                                                                                                                                                       9 RSDHLTT 15
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US-08-466-344-34
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US-09-058-459-1
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| Sequence 34, Application US/08040548 |
| Patent No. 5763209 |
| Patent No. 5763209 |
| Patent No. 5763209 |
| APPLICANT: SUKhatme, Vikas P. |
| TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: WINGTONAL DOMAINS OF DNA BINDING PROTEINS NUMBER OF SEQUENCES: 67 |
| CORRESPONDENCE ADDRESS: ADDRESSE: ATNOIG, White & Durkee STREET: 321 No. 5763209th Clark Street, Suite 800 |
| CITY: Chicago |
| STATE: Illinois |
| COUNTRY: US.A. |
| COMPUTER FRADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 |
| CURRENT APPLICATION DATE: US/08/040,548 |
| APPLICATION NUMBER: US/08/040,548 |
| APPLICATION NUMBER: US/08/040,548 |
| COMPUTER STATE: US/08/040,548 |
| CURRENT APPLICATION DATE: US/08/040,548 |
| COMPUTER STATE: US/08/040,548 |
| CURRENT APPLICATION DATE: US/08/040,548 |
| COMPUTER STATE: US/08/040,548 |
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100.0%; Score 7; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,151
FILING DATE: 22-MAR-1996
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen L.
REGISTRATION NUMBER: 36,675
REFERENCE/COKET NUMBER: 85,97/6
TELEPHONE: 312-321,4200
     ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COUGHLIA, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELEPHONE: (112) 744-090
TELEPAX: (312) 245-4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-151-111
                                                              STREET: Plaza Dri
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-09-037-179B-15
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
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Mayo, Stephen L.

"FPLICANT: Dahiyat, Bassil I.

"FPLICANT: Gordon, D. B.

APPLICANT: Street, Arthur

TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
FILE REPRENSE: A6533-3/RET/RMS/SJR

FILE REPRENSE: B6533-3/RET/RMS/SJR

CURRENT APPLICATION NUMBER: U5/09/058,459

CURRENT FILING DATE: 1907-04-10

PRIOR APPLICATION NUMBER: 60/043,464

PRIOR FILING DATE: 1997-04-11

PRIOR FILING DATE: 1997-04-11

PRIOR FILING DATE: 1997-04-04

NUMBER: 60/061,097

PRIOR FILING DATE: 1997-10-03

NUMBER: PATENTION NUMBER: 60/061,097

PRIOR FILING DATE: 1997-10-03

NUMBER: PATENTION NUMBER: 60/061,097

PRIOR FILING DATE: 1997-10-03

NUMBER: PATENTION NUMBER: 60/061,097

PRIOR FILING DATE: 1997-10-03

TENGTH: 28

TYPE: pr.
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APPLICANT: Mayo, Stephen L.

APPLICANT: Dahiyat, Bassil L.

APPLICANT: Gordon, D. Benjamin

APPLICANT: Street, Arthur

APPLICANT: Apparatus and Method for Automated Protein Design

TITLE OF INVENTION: Apparatus and Method for Automated Protein Design

TITLE OF INVENTION: Apparatus and Method for Automated Protein Design

FILE REPERENCE: A65353-4/RFT/RMS/SJR

CURRENT FILING DATE: 1998-07-31

PRIOR PELING DATE: 1997-04-11

PRIOR PPLICATION NUMBER: 60/061,097

PRIOR PPLICATION NUMBER: 60/061,097

PRIOR PPLING DATE: 1999-04-10

PRIOR PLING DATE: 1998-04-10

PRIOR PLING DATE: 1998-04-10

PRIOR PLING DATE: 1998-06-01

NUMBER: OF SEQ ID NOS: 99

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 1

LENGTH: 28
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Patent No. 6269312
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Mouse
US-09-058-459-1
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US-09-240-179-2

Sequence 2, Application US/09240179

Sequence 2, Application US/09240179

Batent No. 6410248

GENERAL INPORTATION

APPLICANT: Pabo, Carl O.

APPLICANT: Pabo, Carl O.

APPLICANT: Pabo, Carl O.

APPLICANT: Pabo, Carl O.

TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc

TITLE OF INVENTION: Pinger Proteins for Diverse DNA Target Sites

FILE REFERENCE: 019496-0002200S

CURRENT APPLICATION NUMBER: US/09/240,179

CURRENT FILING DATE: 1999-01-29

BARLIER PILING DATE: 1999-01-30

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 28

LENGTH: 28
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OTHER INFORMATION: Description of Artificial Sequence: Zif268 zinc; OTHER INFORMATION: finger 2
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Bruening, Wendy
APPLICANT: Bruening, Wendy
APPLICANT: Bruening, Wendy
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
FILE REFERENCE: 0050.1312-011
CURRENT FILING DATE: 1998-03-09
PRIOR PELLING DATE: 1998-03-09
PRIOR PILING DATE: 1998-03-09
PRIOR PILING DATE: 1998-11-13
PRIOR PILING DATE: 1999-11-13
PRIOR FILING DATE: 1999-11-13
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Sequence 15, Application US/09037179B Patent No. 6216599 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                             Pelletier, Jerry
Haber, Daniel A.
Rose, Elise A.
Housman, David E.
Bruening, Wendy
                                                                                          APPLICANT: Call, Katherine M. APPLICANT: Glaser, Thomas M. APPLICANT: Ito, Caryn Y. APPLICANT: Buckler, Alan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Est Local Similarity 77, Conservative
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US-09-714-357-1
; Sequence 1, Application US/09714357
; Patent No. 6708120
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Street, Arthur
; TITLE OF INVENITON: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; TILE OF INVENITON: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; TILE REFRENCE: A65353-3/RFT/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/714,357
; CURRENT APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR PELING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PATENTIN VET: 2.1
; SEQ ID NO 1
                                               Gaps
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Query Match 100.0%; Score 7; DB 4; Length 28; Best Local Similarity 100.0%; Pred. No. 0.043; Matches 7; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Mouse
US-09-714-357-1
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Patent No. 6503717
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Edward J.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REPERENCE: 019496-002310US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR APPLICATION NUMBER: US 09/456,100
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                          December 27, 2004, 19:21:38; Search time 15.85 Seconds (without alignments) 29.289 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Score Match Length DB
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LENGTH: 7
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Sequence:
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No.
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CRGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:SBS11

OTHER INFORMATION: recognition helix

US-09-731-558-22

Query Match

Best Local Similarity 100.0%; Score 7; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.86+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 DRSHLAR 7

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Db 1 DRSHLAR 7

Search completed: December 27, 2004, 20:31:02
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Fatent No. 6794136

GENERAL INFORMATION:
APPLICANT: EISBNERG, Stephen P.
APPLICANT: REBAR, Edward
APPLICANT: REPARTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT PRILIG DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PALENTH Ver. 2.0
SEQ ID NO 30
LENGTH: 7
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                                                                                                                                     December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29:197 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 4 US-09-716-637-30
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                                                                                              OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                 US-09-846-033B-77
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Score Match Length DB
                                                                                                                                                                                                                                                                                       1 RSDNLQR 7
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US-09-716-637-30
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No.
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; OTHER INFORMATION: Description of Artificial Sequence: VEGF-II US-09-716-637-30
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                                                                                          Indels
                                                       Length 7;
                                                     Query Match
100.0%; Score 7; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0;
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ne : 24.9 secs
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Job time
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Sequence 30, Appl
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Fatent No. 6794136

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: JAMIESON, Andrew

APPLICANT: REBAR, Edward

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 8325-0020

CURRENT APPLICANT: 2001-10-12

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PALENTIN VET. 2.00

SEQ ID NO 30

LENGTH: 7

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  December 27, 2004, 18:12:11; Search time 15.9 Seconds (without alignments) 29:197 Million cell updates/sec
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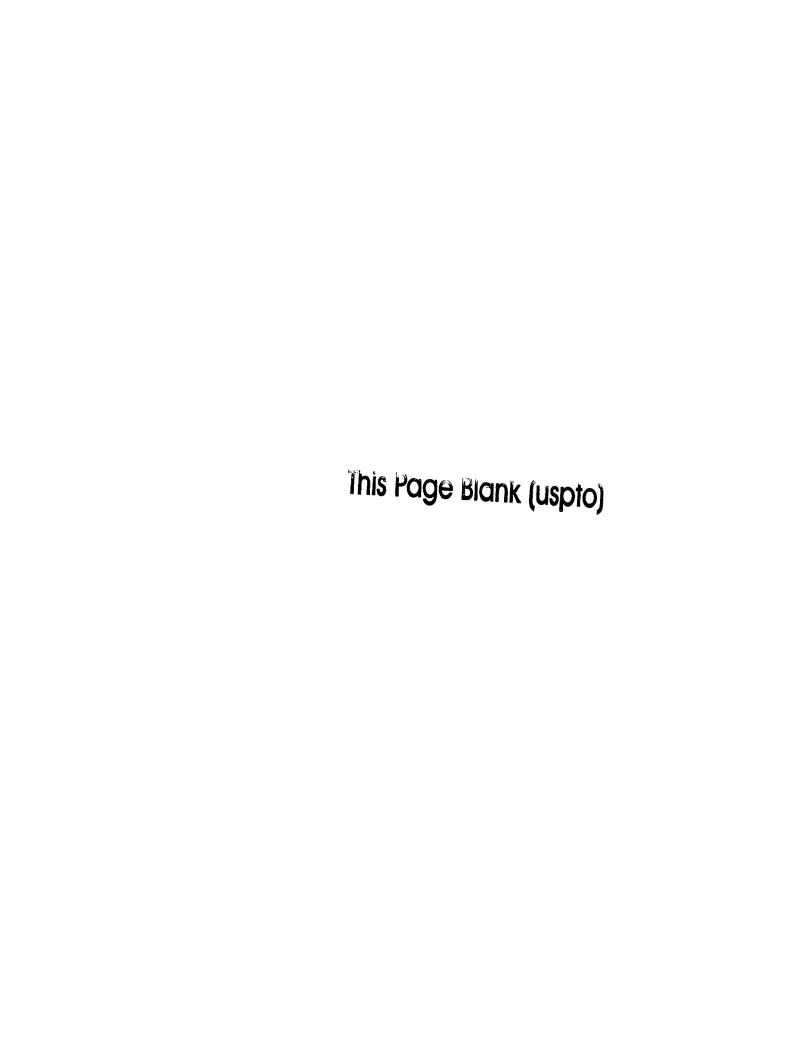
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                           US-09-846-033B-76
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Maximum DB seq length: 200000000
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Score Match Length DB
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, OTHER INFORMATION: Description of Artificial Sequence: VEGF-II
US-09-716-637-30
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                                                                Ouery Match

100.0%; Score 7; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                               December 27, 2004, 18:12:11 ; Search time 15.9 Seconds (without alignments) 29:197 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents AA:*
1: /cgn2 6/ptodata1/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 4 US-09-716-637-30
                                                                                                                                                                                                                                                                                   478139 seqs, 66318000 residues
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                                                                 OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                               US-09-846-033B-75
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Score Match Length DB
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Perfect score:
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; OTHER INFORMATION: Description of Artificial Sequence: VEGF-II US-09-716-637-30
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                                                                                                    Indels
                                                              Length 7;
                                                            Query Match
100.0%; Score 7; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0;
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1 RSDNLOR

Search completed: December 27, 2004, 19:21:24 Job time : 15.9 secs

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                                                                                                         RESULT 8

US-09-478-681-30

| Sequence 30, Application US/09478681
| Patent No. 6607882
| GENERAL INFORMATION:
| APPLICANT: Cox III, George N. APPLICANT: Case, Case, Casey Christopher APPLICANT: Stratt, Sharon K. TILE OF INVENTION: USING ZINC FINGER PROTEINS
| TILE OF INVENTION: USING ZINC FINGER PROTEINS
| TILE OF INVENTION: USING ZINC FINGER PROTEINS
| TILE REPRENCE: BA32-0002.10 / S2-US3
| CURRENT APPLICATION UNBER: US/09/478,681
| CURRENT FILING DATE: 2000-01-06
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: PATENTIN Ver. 2.0
| SEQ ID NO 30
| LENGTH: 196
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US-09-779-233-18
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233

Patent No. 6689558

GENERAL INFORMATION:

APPLICANT: Case, Casey,

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REPRENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT APPLICATION NUMBER: 201-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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178 RSDHLSR 184
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1 RSDHLSR 7
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Search completed: December 27, 2004, 21:40:39 Job time : 16.35 secs

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Sequence Sequence

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Sequence 1 Sequence 1

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Sequence:

Database :

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Description of Artificial Sequence: recognition helix
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
US-09-989-789-840
US-09-989-789-1001
US-09-989-789-1001
US-09-989-789-1009
US-09-989-789-1009
US-09-989-789-1009
US-09-989-789-1138
US-09-989-789-1138
US-09-989-789-1139
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US-09-989-789-1535
US-09-989-789-1135
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Patent No. US20020045158A1
GENERAL INFORMATION:
APPLICANT: Case, Case, Case, TITLE OF INVENTION:
FILE REFERENCE: 8325-0010
CURRENT APPLICANTION NUMBER: US/09/779,233
CURRENT FILING DATE: 2011-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 229, Application US/09989789
Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Matches 7; Conser
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US-09-989-789-229
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                                                                                                                                                    December 27, 2004, 19:43:18; Search time 52.7 Seconds (without alignments) 47.701 Million cell updates/sec
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2: (cgm2_6/ptodata/2/pubpaa/Der/ NEW PUB.pep:*
3: (cgm2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
3: (cgm2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: (cgm2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: (cgm2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: (cgm2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: (cgm2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
9: (cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: (cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
10: (cgm2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: (cgm2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
12: (cgm2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
13: (cgm2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
14: (cgm2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
15: (cgm2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
16: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
17: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
18: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
19: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
10: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
10: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
10: (cgm2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-989-789-229
US-09-989-789-234
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US-09-989-789-239
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US-09-989-789-426
US-09-989-789-426
US-09-989-789-426
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US-09-989-789-426
US-09-989-789-428
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                                                                                                                  protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                 US-09-846-033B-109
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Maximum DB seq length: 200000000
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Match Length
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Result

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Sequence 239, Application US/09989789
Factor No. US20020063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPILICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCES: 8325-0011.20 / 811-US2
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOCTHARE: PATENTIN VET. 2.0
SEQ ID NO 239
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 238, Application US/09989789
Fatent No. US2002006337941
Fatent No. US2002006337941
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE REFERENCE: 8325-0011.20 / $11.052
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER: OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-238
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                                                                             Length 7;
                                                                         100.0%; Score 7; DB 9; Lt 100.0%; Pred. No. 1.4e+06;
                                                                                                                                               0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 10v..
7; Conservative
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                                             Query Match
Best Local Similarity
7, Conserve
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US-09-989-789-239
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              US-09-989-789-234
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Sequence 20, Application US/09989789
Parent No. US20020063379A1
GENERAL INFORMATION:
APPLICAMT: LIJU, QABA
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8125-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4065
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 230
LENGTH: APPLICATION OF CONTROL OF
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Patent No. US20020063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCE: 8325-0011.20 / S11-US2
CURRENT APPLICAND NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 234
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS FILE REFERENCE: 8325-0011.20 / S11-US2 CURRENT APPLICATION NUMBER: US/09/989,789 CURRENT FILING DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4085 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 229
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Best Local Similarity 100.
Matches 7; Conservative
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) OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-425
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-989-789-426
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Sequence 425. Application US/09989789

Parent No. US20020063379A1

GENERAL INFORMATION:

APPLICANT: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989, 789

CURRENT APPLICATION DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PatentIn Ver. 2.0
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US-09-989-789-420

US-09-989-789-420

Sequence 420, Application US/09989789

Patent No. US20020063379A1

GENERAL INFORMATION:

APPLICANT: LIU, Olang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / 811-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PATENTIN VET. 2.0
                                                              APPLICANT: LIU, GLANGE TITLE OF INVENTION DEPENDENT RECOGNITION OF GNN NUCLECTIDE TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 244
LENGTH: 7
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Sequence 244, Application US/09989789
Patent No. US20020063379A1
GENERAL INFORMATION:
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Best Local Similarity 100...
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Matches 7; Conservative
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Patent No. US2002063379A1

GENERAL INFORMATION:

APPLICANT: LIU Qiang

TITLE OF INVENTION:

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 428
                                                                                                                                                                                                                                                   Sequence 426, Application US/09989789
Patent No. US20020063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER: OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 426
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Length 7;
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100.0%; Score 7; DB 9; L. 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0;
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ORGANISM: Artificial Seguence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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     Sequence 434, Application US/09989789

Patent No. US20020063379A1

GENERAL INFORMATION:

APPLICANT: LIU, Qiang

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 434
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Betent No. US200200337941

GENERAL INFORMATION:

APPLICANT: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT PLING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0
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Patent No. US20020063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCE: 8125-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
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100.0%; Score 7; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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1 RSDHLSR 7
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US-09-989-789-840
US-09-989-789-434
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Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8125-0011.20 / 811-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-888
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                    0; Mismatches
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                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 840
LENGTH: 7
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Best Local Similarity 100.
Matches 7; Conservative
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Word size :

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Title: Perfect score:

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Sequence:

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Sequence 29, Application US/09716637

Sequence 29, Application US/09716637

Batent No. 6794136

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: APPLICANT: Andrew

APPLICANT: REBAR, Edward

TITLE OF INVENTION: IPERATIVE OPTIMIZATION IN THE DESIGN OF BINDING

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 8325-0020

CURRENT FILING DATE: 200-10-12

NUMBER OF SEQ ID NOS: 35

SOFTWARE PARENCE: 200-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix
                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
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US-09-779-233-44

i Sequence 44, Application US/09779233

i Patent No. 668958

i GENERAL INFORMATION:

i APPLICANT: Case, Casey

i TILLE OF INVENTION:

FILE REFERENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

i NUMBER OF SEQ ID NOS: 45

i SOFTWARE: PatentIN Ver. 2.0

i SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
CURRENT FILING DATE: 2000-12-06
PRIOR PAPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SECTIVARE: Patentin Ver: 2.1
SEQ ID NO 14
                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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1 RSDHLSR 7
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LENGTH: 7
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Sequence 17, Application US/09731558

Bratent No. 6503717

GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Bangame Blosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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28.393 Million cell updates/sec
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Sequence 29,
Sequence 15,
Sequence 15,
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Sequence 30,
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                                                                                                                                                             December 27, 2004, 20:31:09; Search time 16.35 Seconds
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2: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-49
US-09-229-037-15
US-09-779-233-3
US-09-478-681-15
US-09-478-681-30
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                                                                                                                    OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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US-09-731-558-14

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| General NO. 00394201
| General INFORMATION:
| APPLICANT: Case, Casey Christopher
| APPLICANT: Elsemberg, Stephen P.
| APPLICANT: Elsemberg, Stephen P.
| APPLICANT: Spratt, Sharon Kaye
| APPLICANT: Sangamo Biosciences, Inc.
| APPLICANT: Sangamo Biosciences, Inc.
| TITLE OF INVENTION: Elsembers, Inc.
| TITLE OF INVENTION: Elsembers Display of Endogenous Gene Expression in Cells Using
| TITLE OF INVENTION: Zinc Finger Proteins
| TITLE OF INVENTION STATE FIGURES: US/09/229,037A
| CURRENT PILING DATE: 1999-01-12
| NUMBER OF SEQ ID NOS: 140
| SOFTWARE: Patentin Ver. 2.0
| SEG ID NO. 30
; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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; OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30
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                                                                                                       Length 99
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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches
                                                                                                       100.0%; Score 7; DB 4; 100.0%; Pred. No. 0.16;
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; Sequence 3, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
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ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Jarvis, Eric Edward
APPLICANT: Sngamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Cox III, George N.
APPLICANT: Case, Casey Christopher
APPLICANT: Edsenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 8325-0002.10 / S2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
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                  ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP
                                                                                                         100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; ive 0; Mismatches 0; Indels
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Sequence 15, Application US/09229037A
Patent No. 6534261
GENERAL INFORMATION:
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US-03-478-681-15
'Sequence 15, Application US/09478681
'Patent No. 6607882
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ORGANISM: Artificial Sequence
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SEQ ID NO 15
LENGTH: 99
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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LENGTH: 99
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Sequence 30, Application US/09478681

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Sequence 30, Application US/09478681

Sequence 30, Application US/09478681

Sequence 30, Application US 607882

APPLICANT: Case, Casey Christopher

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Brenberg, Stephen P.

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REGILATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZING FINGER PROTEINS

FILE REFERENCE: 8325-0002.10 / S2-US3

CURRENT PAPLICANT: ON UMBER: US/09/478, 681

CURRENT PAPLICANT: 2.0

SEQ ID NO 30

LENGTH: 196

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 7; DB 4; Length 196; Best Local Similarity 100.0%; Pred. No. 0.3; Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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US-09-779-233-18
Sequence 18, Application US/09779233
Patent No. 668958
GENERAL INFORMATION:
APPLICANT: Case,
TILLE OF INVENTION:
FILE REPERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779, 233
CURRENT APPLICATION NUMBER: 201-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: December 27, 2004, 21:40:38 Job time : 16.35 secs
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 RSDHLSR 184
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                                          178 RSDHLSR 184
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LENGTH: 196
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RESULT 2
US-09-779-233-37
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Sequence 17, Application US/09731558

Patent No. 6503717

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Liu, Qiang

APPLICANT: Liu, Qiang

APPLICANT: Rebar, Edward J.

TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger

TITLE OF INVENTION: Proteins for the Identification of Gene Function

TITLE OF INVENTION: Proteins for the Identification of Gene Function

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REPRENCE: 019496-003210US

CURRENT APPLICATION NUMBER: US 09/456,100

PRIOR APPLICATION NUMBER: US 09/456,100

PRIOR APPLICATION NUMBER: US 09/456,100

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17
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Sequence 37, Appl
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                                                                                                                                                                                   (without alignments)
28.393 Million cell updates/sec
                                                                                                                                                          December 27, 2004, 20:31:09; Search time 16.35 Seconds
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-731-558-17
US-09-779-233-37
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                                                                                                        OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Score Match Length DB
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US-09-731-558-17
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                                               ) OTHER INFORMATION: Description of Artificial Sequence:SBS6; OTHER INFORMATION: recognition helix US-09-731-558-17
                                                                                                                                             Query Match

100.0%; Score 7; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/09779233
Patent No. 668958
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8235-0010
CURRENT PAPLICATION NUMBER: US/09/779,233
CURRENT PILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: December 27, 2004, 21:40:39 Job time : 16.35 secs
ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
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Length 7;

Title: Perfect score:

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Scoring table:

Word size :

Searched:

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APPLICANT: EISENBERG, Stephen P.
APPLICANT: EISENBERG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: REBAR, Edward
TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DATE: 2001-10-12
SOFTWARE: PATENTIN VOS: 2.0
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                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
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Sequence 44, Application US/09779233

Sequence 44, Application US/09779233

Patent No. 6689558

Three OF INVENTY Case, Casey

TITLE OF INVENTYION: CELLS FOR DRUG DISCOVERY

FILE REFERENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 44
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 7
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ORGANISM: Artificial Sequence
                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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Matches 7; Conservative
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1 RSDHLSR 7
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Sequence 49, Appl
Sequence 29, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 19, Appl
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Sequence 14, Application US/09731558
Patent No. 650317
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Sangame Blosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
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                                                                                                                                                                               December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec
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2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-716-637-29
US-09-229-037-15
US-09-779-233-3
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-478-681-30
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                                                                                                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                 US-09-846-033B-111
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Maximum DB seq length: 200000000
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Match Length DB
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Score

8 Result

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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cas, Casey Christopher
APPLICANT: Cas, Casey Christopher
APPLICANT: Gas, Casey Christopher
APPLICANT: Brands Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Spangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
ANUMER OF SEQ ID NUMBER: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter
US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1 US-09-779-233-3
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OTHER INFORMATION: Description of Artificial Sequence:designed

OTHER INFORMATION: 6-finger ZPP VEGF3a/1 from KpnI to BamHI
US-09-229-037-30
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                            Length 99
                                                                                                                                             ilarity 100.0%; Score 7; DB 4;
Conservative 0; Mismatches
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; Sequence 3, Application US/09779233
; Sequence 3, Application US/09779233
; GENERAL INFORMATION:
; APPLICANT: Case, Case,
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; TITLE REPREBREE: 8325-0010
; CURRENT APPLICATION UNMER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 99
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100.0%; Pred. No. 0.16;
vative 0; Mismatches
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US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
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ORGANISM: Artificial Sequence
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81 RSDHLSR 87
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Baronkay
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
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| GENERAL INFORMATION:
| APPLICANT: Case, Casey Christopher
| APPLICANT: Case, Casey Christopher
| APPLICANT: Eisenberg, Stephen P.
| APPLICANT: Eisenberg, Stephen P.
| APPLICANT: Spratt, Shrit E.
| APPLICANT: Shrit E.
| APPLICANT: Spratt, Shrit E.
| APPLICANT: Shrit E.
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| APPLICANT: Shrit E
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                        , FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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                                                                                                                                                               Length 7;
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100.0%; Score 7; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0;
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; Sequence 15, Application US/09229037A
; Patent No. 6534261
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; Sequence 15, Application US/09478681
; Patent No. 6607882
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Best Local Similarity
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LENGTH: 99
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Spratt, Sharon K.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION CENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 8325-6002.10 / S2-US3
CURRENT APPLICANTION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SSQ ID NO 30
: SEQ ID NO 30
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OTHER INFORMATION: Description of Artificial Sequence:designed
CHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI
US-09-478-681-30
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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233

Patent No. 6689558

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REPRENCE: 8325-0010

CURRENT APPLICATION WUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 196
                                                                                     RESULT 8
US-09-478-681-30
; Sequence 30, Application US/09478681
; Patent No. 6607882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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178 RSDHLSR 184
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178 RSDHLSR 184
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; Patent No. 622504
; GENERAL INFORMATION:
    APPLICANT: Briatol-Myers Squibb, Co.
    APPLICANT: Brandt, Petra
    APPLICANT: Brandt, Petra
    APPLICANT: Brandt, Petra
    APPLICANT: Cano, Paul M
    APPLICANT: Cano, Paul M
    APPLICANT: Goldberg, Steven L
    APPLICANT: Modlberg, Steven L
    APPLICANT: Modlberg, Steven L
    APPLICANT: Mueller, Goachim
    APPLICANT: Mueller, Joachim
    APPLICANT: Mueller, Joachim
    APPLICANT: Mueller, Goachim
    APPLICANT: Petrebabach, Hans
    TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
    TITLE OF INVENTION: NUMBER: US/09/413,814
; CURRENT APPLICATION NUMBER: US/09/413,814
; CURRENT FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44, Appl
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                                                                                                                                                            December 27, 2004, 20:31:09 ; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec
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2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Score Match Length DB
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No.
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; EARLIER APPLICATION NUMBER: DE 198 46 493.2
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 881
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-44

Query Match

De 295 RSDALAR 7

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| Db 295 RSDALAR 301

Search completed: December 27, 2004, 21:40:39
Job time: 16.35 secs
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Word size :

Database

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Searched:

Sequence:

Run on:

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APPLICANT: EISENBERG, Stephen P.
APPLICANT: EISENBERG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: REBAR, Edward
TITLE OF INVENTION: TERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REPERBENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DAFE: 2001-10-12
SOFTWARE: PATENTIN OFF: 2.0
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Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
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Facent No. 669958
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT APPLICATION NUMBER: US/09/779,233
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
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                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 7
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-779-233-44
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Sequence 29, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 18, Appl
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Sequence 14, Application US/09731558
Patent NO. 6503717
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Liu, Qiang
APPLICANT: Sangame Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019946-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
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28.393 Million cell updates/sec
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2: /cgn2 6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2 6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2 6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2 6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2 6/prodata/1/iaa/PCTUS COMB.pep:*
                                                      Compugen Ltd.
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US-09-779-233-44
US-09-779-233-41
US-09-229-037-15
US-09-779-233-3
US-09-478-681-30
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US-09-779-233-18
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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                                                                                                                                                                                                                                                             US-09-846-033B-109
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Maximum DB seq length: 200000000
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Match Length DB
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Gaps

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GENERAL INFORMATION:
APPLICANT: Cas III, George No. 6534261bert
APPLICANT: Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Bravis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Ene Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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                                                                                          Length 99;
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Sequence 3, Application US/09779233

Patent No. 6689558

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REFERENCE: 3255-601

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 99
                                                                              100.0%; Score 7; DB 4; ilarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
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100.0%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches
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81 RSDHLSR 87
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Best Local Similarity
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APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Jarvis, Eric Edward
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cox III, George N.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Blandberg, Stephen P.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 99
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// FEATURE:
// OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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                                                                                            100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.88+05;
                                                                                                                                           0; Mismatches
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; Sequence 15, Application US/09229037A
; Patent No. 6534261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-478-681-15
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LENGTH: 99
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Sequence 19, Application US/09614679A
Patent No. 6492117
GENERAL INPORMATION:
APPLICANT: CHOO, YEN
APPLICANT: ISALAN, MARK
APPLICANT: BALASUBRAMANIAN, SHANKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09139762A Patent No. 6013453 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-614-679A-19
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Sequence 1, Appli
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                                                                                                                      December 27, 2004, 17:02:31; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
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Sequence 1, Ap
Sequence 1, Ap
Sequence 1, Ap
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/cgn2 6/ptodata/1/iaa/5B COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-139-762A-19
US-08-040-548-19
US-08-466-344-19
US-09-229-007A-95
US-10-113-424-95
US-10-113-424-95
US-08-620-151-111
US-08-620-151-111
US-08-620-151-111
US-08-058-459-1
US-09-058-459-1
US-09-127-926-1
US-09-127-926-1
US-09-137-179B-15
US-09-17-926-1
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US-09-17-926-1
US-09-17-928-1
US-09-17-928-1
US-09-116-637-1
US-08-46-348-7
US-08-46-348-7
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US-09-229-007A-8
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US-10-057-552-1
US-08-040-548-8
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US-08-676-318A-5
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                                                                                          OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Sequence 44, Appl
Sequence 8, Appli
Sequence 1278, Ap
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Sequence 2, Appli
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Sequence 36,
Sequence 44,
                       Sequence
                                                                                  Sequence
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                                                                Sequence
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APPLICANT: Choo, Yen
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Length 7;
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100.0%; Pred. No. 3.8e+05;
ive 0; Mismatches 0;
US-09-500-700-5
US-08-224-482-11
US-08-863-813A-34
US-08-676-318A-34
US-08-676-318A-36
US-09-500-700-34
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US-08-224-482-8
US-08-24-482-8
US-08-24-66-348-2
US-08-46-348-2
US-08-46-348-2
US-08-46-348-2
US-08-46-348-2
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APPLICANT: BALASUBRAMANIAN, SHANKAR
APPLICANT: LIU, XIAOHAI
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 71278/271599
CURRENT APPLICATION NUMBER: US/09/614,679A
CURRENT FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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Gaps
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Sequence 19, Application US/08040548

Setent No. 5763209

GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS

NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: 321 No. 5763209th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; DB 3; Length lu;
100.0%; Pred. No. 0.017; "..matrches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COUGHII, Daniel F.
REGISTRATION NUMBER: 35,111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-ANG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-491
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown; MOLECULE TYPE: peptide US-09-139-762A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-040-548-19
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                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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US-09-139-762A-53
Squarec 53, Application US/09139762A
Fatent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: US -UN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG 1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
BROWNER: 08-9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ 1D NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                          ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
COMPUTER: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-UUN-1997
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Best Local Similarity 100.
Matches 7; Conservative
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FILE REFERENCE: 019496-001800US
CURRENT APPLICATION NUMBER: US/09/229,007A
CURRENT FILING DATE: 1989-01-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 95
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 95, Application US/10113424
Patent No. 6785613
GENERAL INFORMATION:
APPLICANT: Eisenberg, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
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R RSDHLTT 14
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Best Local Similarity
Matches 7; Conserv
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US-08-620-151-111
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APPLICANT: Elsenberg, Casey C.
APPLICANT: Case, Casey C.
APPLICANT: Cox III, George N.
APPLICANT: Jamieson, Andrew
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
TITLE OF INVENTION: to Bind to Preselected Sites
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; DB 1; Length 20; 100.0%; Pred. No. 0.031; cive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FLING DATE:

CLASSIFICATION NUMBER:

CLASSIFICATION NUMBER:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60610
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-229-007A-95; Sequence 95, Application US/09229007A; Sequence 95, Application US/09229007A; Setent No. 6453242; GENERAL INFORMATION:
                                                                                                                                                                                                       ; Sequence 19, Application US/08466344; Patent No. 5773583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||||
9 RSDHLTT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSDHLTT 7
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                                                                                                                                                              RESULT 5
US-08-466-344-19
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APPLICANT: Case, Casey C.

APPLICANT: Case, Casey C.

APPLICANT: Case C.

APPLICANT: Case C.

APPLICANT: Jamieson, Andrew

APPLICANT: Sangame Biosciences, Inc.

APPLICANT: Sangame Biosciences, Inc.

APPLICANT: Sangame Biosciences, Inc.

TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger

TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger

TITLE OF INVENTION: Designing Zinc Finger

TITLE OF INVENTION: Designing Zinc Finger

TITLE OF INVENTION: US/10/113,424

CURRENT APPLICATION NUMBER: US/10/113,424

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 97

SEQ ID NO 95

LENGTH: 21
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US-10-113-424-95
) OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence; OTHER INFORMATION: (F1, F2 and F3) from Zif 268
US-09-229-007A-95
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Patent No. 5928955
GENERAL INFORMATION:
APPLICANT: Imperial; Barbara
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVALENT ZINC
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 7; DB 4; Length 21; 100.0%; Pred. No. 0.033; ive 0; Mismatches 0; Indels
                                                                                                                         Length 21;
                                                                                                                         100.0%; Score 7; DB 4; Le
100.0%; Pred. No. 0.033;
tive 0; Mismatches 0;
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Gaps

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Sequence 34, Application US/08466344

Patent No. 5773583

GENERAL INFORMATION:
APPLICANT: SUKhatume, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS; NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 1; Length 28; 100.0%; Pred. No. 0.043; Live 0; Mismatches 0; Indels
                                                                                                                                                                                          100.0%; Score 7; DB 1; Length 28; 100.0%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv...
7; Conservative
                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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US-08-466-344-34
                                                                                                                                                            US-08-040-548-34
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US-09-058-459-1
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Sequence 34, Application US/08040548

Patent No. 5763209

SEQUENCE IN O. 5763209

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS

TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: 321 No. 5763209th Clark Street, Suite 800

CITY: Chicago

STRATE: 111inois

CONDITRY: U.S.A.

ZIP: 60610

CONDITRY: U.S.A.

MEDIUM TYPE: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DAMBER: US/08/040,548
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ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: 111inois
CONFUTRY: USA
ZIP: 60611-5599
COMPUTRY: LIB PC Compatible
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,151
FILING DATE: 22-MAR-1996
CLASSIFICATION: A22
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen D.
REFERENCE/DOCKET NUMBER: 36,675
REFERENCE/DOCKET NUMBER: 36,675
REFERENCE TALON
TELEPHONE: 312-321-4299
INFORMATION FOR SEQ ID NO: 111:
SEQUENTE AMINO ACIDS
SEQUENTE AMINO ACIDS
TELEFAX: LA20
TELEFAX: LA20
TELEFAX: LA20
TELEFAX: A12-321-4299
INFORMATION FOR SEQ ID NO: 111:
SEQUENTE: Camino acids
TYPE: amino acids
TYPE: amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: COUGHLIA, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELEPHONE: (112) 744-090
TELEPHONE: (312) 245-4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-620-151-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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ORGANISM: Homo sapien
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LENGTH: 28
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                                                              APPLICANT: Mayo, Stephen L.
APPLICANT: Mayo, Stephen L.
APPLICANT: Dahlyat, Bassil I.
APPLICANT: Gordon, D. B.
APPLICANT: Gordon, D. B.
TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
FILE REFERENCE: A65383-3/RFT/RMS/SJR
FILE REFERENCE: A65383-3/RFT/RMS/SJR
CURRENT FILING DATE: 1097-000-04-10
PRIOR APPLICATION NUMBER: 60/043,464
PRIOR APPLICATION NUMBER: 60/054,678
PRIOR APPLICATION NUMBER: 60/054,678
PRIOR FILING DATE: 1997-08-04
SOFTWARE: PACHULIN VEY: 2.1
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APPLICANT: Dahiyat, Bassil L.
APPLICANT: Gordon, D. Benjamin
APPLICANT: Gordon, D. Benjamin
APPLICANT: Gordon, D. Benjamin
APPLICANT: Street, Arthur
APPLICANT: Street, Arthur
APPLICANT: Su, Yaoying
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
TILLE REFERENCE: A65353-4(RFT/RMS/SJR
CURRENT FILING DATE: 1999-07-31
PRIOR FILING DATE: 1997-04-11
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1997-10-03
PRIOR PILING DATE: 1999-04-10
PRIOR PILING DATE: 1999-04-10
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Patent No. 6269312
GENERAL INFORMATION:
Sequence 1, Application US/09058459
Patent No. 6188965
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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ORGANISM: Mouse
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LENGTH: 28
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Securior 12, Apilication US/090311998

GENERAL INFORMATION:

APPLICANT Gall. Katherine M. Gall. Katherine M. APPLICANT Gall. Katherine M. Gall. Gall. M. Gall
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US-09-714-357-1
is Sequence 1, Application US/09714357
patent No. 6708120
is GENERAL INFORMATION:
APPLICANT: Mayo, Stephen L.
APPLICANT: Danlyat, Baseil I.
APPLICANT: Danlyat, Baseil I.
APPLICANT: Danlyat, Baseil I.
APPLICANT: Street, Arthur
ITLE OF INVENTION: APPRARTUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
FILE REFERENCE: AG5153-3/RFT/RMS/SJR
FILE REFERENCE: AG5153-3/RFT/RMS/SJR
CURRENT APPLICATION NUMBER: 09/09/9/714,357
CURRENT FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-10
PRIOR PELING DATE: 1997-08-04
PRIOR APPLICATION NUMBER: 60/054,678
PRIOR APPLICATION NUMBER: 60/061,097
PRIOR PELING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 1
LENTH: 28
                                                  0; Gaps
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Query Match 100.0%; Score 7; DB 4; Length 28; Best Local Similarity 100.0%; Pred. No. 0.043; Matches 7; Conservative 0; Mismatches 0; Indels
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13 RSDHLTT 19
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CRGANISM: Mouse
US-09-714-357-1
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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December 27, 2004, 17:02:31 ; Search time 15.8 Seconds (without alignments) 29.381 Million cell updates/sec
OM protein - protein search, using sw model
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US-09-846-033B-30 Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 1 RSDHLAR Scoring table: Sequence:

478139 segs, 66318000 residues

Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

1: /cgn2 6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:* Issued Patents AA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Search completed: December 27, 2004, 18:12:02 Job time : 16.8 secs

57 RSDHLAR 63

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Description	Sequence 42, Appl Sequence 16192, A
ID	1 7 100.0 7 4 US-09-779-233-42 Sequence 42, App. 2 7 100.0 100 4 US-09-248-796A-16192 Sequence 16192, A
DB	44
Length	100
* Query Score Match Length DB ID	7 100.0
Score	7
Result No. 8	- 70

ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence: recognition; OTHER INFORMATION: helix
US-09-779-233-42
                                                                                        APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
SOFTWARE: PatentIn Ver. 2.0
                   Sequence 42, Application US/09779233 Patent No. 6689558 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
-09-779-233-42
                                                                                                                                                                                                                                                             SEQ ID NO 42
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RESULT 2
US-09-248-796A-16192
US-09-248-796A-16192

SEQUENCE 16192, Application US/09248796A

PAPLICANT: KG147137

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:

TITLE OF INVENTION: PCR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PCR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WINGER: US/09/248, 796A

CURRENT APPLICATION NUMBER: US 60/074,725

FRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER: OF SEQ ID NOS: 28208

SEQ ID NO 16192

LENGTH: 100
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                                            0; Indels
Score 7; DB 4; Length 7; Pred. No. 3.8e+05;
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100.0%; Score 7; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 7; Conservative 0; Mismatches
Query Match
100.0%; Score 7; DB
Best Local Similarity 100.0%; Pred. No. 3.8
Matches 7; Conservative 0; Mismatches
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US-09-248-796A-16192
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RSDHLAR 7
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OTHER INFORMATION:
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US-09-779-233-42
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Sequence 679, A
Sequence 687, A
Sequence 887, A
Sequence 893, A
Sequence 1382,
Sequence 1382,
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                                                                                                                                                                          December 27, 2004, 17:02:31 ; Search time 51.45 Seconds (without alignments) 48.859 Million cell updates/sec
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1: \( cgn2 \frac{6}\) \text{prodata} \( 2\) \text{Pubbaa} \( Vus07 \) \text{PUBCOMB} \( Ppp: ** \) \( cgn2 \frac{6}\) \text{prodata} \( 2\) \text{Pubbaa} \( Vus07 \frac{6}\) \text{Pubbaa} \( Vus08 \frac{6}\) \text{Pubbaa} \( Vus09 \frac{6}\) \text{Pubbaa} \( Vus010 \frac{6}\) \\ \( Vus012 \frac{6}\) \text{Pubbaa} \( Vus010 \frac{6}\) \( Vus012 \frac{6}\) \\ \( Vus012 \frac{6}\) \text{Pubbaa} \( Vus00 \frac{6}\) \\ \( Vus012 \frac{6}\) \\ \( Vus012 \frac{6}\) \\(
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                        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-989-789-127
US-09-989-789-202
US-09-989-789-679
US-09-989-789-686
US-09-989-789-687
US-09-989-789-894
US-09-989-789-1382
US-09-989-789-1382
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US-09-989-789-1382
US-09-989-789-1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1595201 seqs, 359116952 residues
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                                                                                                                               - protein search, using sw model
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Maximum DB seq length: 200000000
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Sequence 1711, Sequence 1712, Sequence 1747,

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         Sequence 2619, Sequence 2640, Sequence 2641, Sequence 2683, Sequence 2688, Sequence 2689, Sequence 2689, Sequence 2710, Sequence 2689, Sequence 2689, Sequence 2689, Sequence 2689, Sequence 2689, Sequence 2689, Sequence 2710, Sequen
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Sequence 34,
Sequence 38,
                                                                                                                                                                                                                                                                                                                                                                                                                         2580,
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1.4e+06;
US-09-989-789-1748
US-09-989-789-1771
US-09-989-789-1771
US-09-989-789-1775
US-09-989-789-1775
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Patent No. US20020045158A1;
GENERAL INFORMATION:
APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
CURRENT APPLICATION NUMBER: US/09/779,233;
CURRENT FILING DATE: 2011-02-08;
NUMBER OF SEQ ID NOS: 45;
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
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ORGANISM: Artificial Seguence
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Matches 7; Conserv
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Facent No. US20020063379A1

GENERAL INFORMATION:

APPLICANF: LIU, Qiang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION NUMBER: 202-03-25

NUMBER: OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 202

LENGTH: 7
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Patent No. US20020063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRESENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 679
LENGTH: 7
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLECTIDE TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS FILE OF INVENTION: TRIPLETS BY ZINC FINGERS CURRENT APPLICATION NUMBER: US/09/989,789 CURRENT FILING DATE: 2002-03-25 NUMBER OF SEQ ID NOS: 4085 SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-127
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; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-202
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.'
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-989-789-679
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Patent No. US2020063379A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LILIU, Qiang

TITLE OF INVENTION: POSTITON DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION UNMERR: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 687
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Patent No. US20020063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SEQ ID NO 686
LENGTH: 7
LENGTH: 7
LENGTH: 7
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; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-686
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100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
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atrive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Sequence 1711, Application US/09989789

Patent No. US20020063379A1

GENERAL INFORMATION:

APPLICANT: LIU, Qiang

TITLE OF INVENTION: POSTITON DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOOTWARE: PATENTIN Ver. 2.0
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US-09-989-789-1711
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US-09-989-789-1388
                                                       ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-1382
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ORGANISM: Artificial Sequence
                    ORGANISM: Artificial Sequence FEATURE:
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US-09-989-789-1388
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Sequence 1382, Application US/09989789

Patent No. US20020663379A1

GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRESENCE: 8325-0011.20 / S11-US2
CURRENT APPLICAND NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1382
LENGTH: 7
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Patent No. US20020063379A1
GENERAL INCORPATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989, 789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 894
Sequence 893, Application US/09989789
Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: PROSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCE: 8325-0011.20 / S11-US2
CURRENT PILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
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US-09-989-789-893
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US-09-989-789-894
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Sequence 1712, Application US/09989789
Patent No. US2002063379A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LIU, Oiand
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCATION: TRIPLETS BY ZINC FINGERS
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT APPLICATION NUMBER: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1712
LENGTH: 7
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Patent No. US20020063379A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1747
LENGTH: 7
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Sequence 1746, Application US/09989789

Patent No. US20020063379A1

GENERAL INFORMATION:

APPLICANT: LIU, Olang

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIFLETS BY ZINC FINGERS

TITLE REPRENDENCE: 8225-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT APPLICATION DATE: 2002-03-25
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US-09-989-789-1747
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Matches 7; Conservative
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1 RSDHLAR 7
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US-09-989-789-1747
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1771, Application US/09989789
; Patent No. US2002006337941
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: Patentin Ver. 2.0
                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: example ZFP US-09-989-789-1748
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Job time : 52.45 secs
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ORGANISM: Artificial Sequence
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SEQ ID NO 1748
LENGTH: 7
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Best Local Similarity 100.
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NUMBER OF SEQ ID NOS: 4085
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December 27, 2004, 17:02:30 ; Search time 66.75 Seconds (without alignments) 37.620 Million cell updates/sec
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Compugen Ltd.
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GenCore version
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geneseqp2003as:*
geneseqp2003bs:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aae08727 Human KCA	Abb80792 Human ER-		Zinc) Zinc	5 Zinc	3 Zinc	Zinc	2 Zinc	Abp49902 Zinc fing	5 Zinc	Zinc	9 Zinc												
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ALIGNMENTS

RESULT 1

165

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Screening compound for interaction with molecular target by contacting compound with cells, comprising exogenous zinc finger protein that modulates expression of target, and determining values of properties of Human, KCA4; EPO; molecular target; zinc finger protein; ZFP; cellular process; signal transduction; drug-screening. Human KCA4 protein Fl recognition helix. AAE08727 standard; peptide; 7 AA (SANG-) SANGAMO BIOSCIENCES INC. 08-FEB-2001; 2001WO-US004301. 08-FEB-2000; 2000US-0181117P. (first entry) WPI; 2001-522491/57. WO200159450-A2 Homo sapiens. 15-NOV-2001 16-AUG-2001. AAE08727; Case C; AAE0872

Example 10; Page 73; 99pp; English.

The invention relates to a method of screening a compound for interaction with a molecular target. The method involves contacting first and second cells with the compound and determining the values of properties of the compound. The second cell comprises an exogenous zinc finger protein (ZFP) that modulates the expression of the molecular target, or isolating membranes from cell comprising ZFP. The methods allow for high throughput screening of candidate compound and reduces the incidence of false positives. The methods are useful for screening a compound for interaction with a molecular target or for screening a compound for its effect on a cellular process. The method is useful for testing a compound for its capacity to transduce a signal to the molecular target or its capacity to block transduction of a signal through the molecular target,

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Homo sapiens.
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                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                The invention relates to regulating the expression of a gene residing in the chromatin of a cell. The method involves identifying one or more accessible regions in cellular chromatin associated with gene; designing a regulatory molecule, where the regulatory molecule comprises a DNA-binding domain targeted to a sequence within the accessible region, and contacting the regulatory molecule with the cell. The method is used for regulating the expression of a gene (e.g., a gene encoding a nuclear receptor such as estrogen receptor alpha (BRalpha), certogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha (CMRyalpha), papatocyte nuclear factor 4 gamma (HNRyalpha), retinoid X receptor alpha (ARRalpha), constitutively active receptor alpha (CARalpha)).

Calpha (AXRalpha), or constitutively active receptor alpha (CARalpha)) residing in the chromatin of a cell. Regulation of gene expression (such as nuclear receptor games) will be useful in treatment of various chiesase, including cancer, diabetes and cardiovascular disease, where the regulatory molecule as described above, is contacted with the cell to carry out the regulation. The method is also useful for modulation of gene expression for therapeutic or prophylactic applications e.g., diabeter retinopathy, ischaemia, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regulating expression of gene by contacting cell with regulatory molecule comprising DNA-binding domain targeted to sequence within accessible region of cellular chromatin associated with a gene, and functional
                                                                                                                                                                                                                                                                                                                                               ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin; gene expression; antirheumatic; antiarthritic; antipsoriatic; nootropic; neuroprotective; estrogen receptor alpha; ER-alpha;
                                                                                                              Gaps
and for performing biochemical drug-screening assays. The present sequence is human KCa4 protein recognition helix used in the exemplification of the invention
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                                                                                   Length 7;
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                     ABB80792 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SANG-) SANGAMO BIOSCIENCES INC
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                                                                    Query Match
Beet Local Similarity 100.v.
Beet Local Similarity 7; Conservative
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disease, stroke, etc. The method also has applications in pharmaceutical research of both nuclear receptors of known function as well as those of unknown function. The method also facilitates development of tissue and animal models of disease states, drug validation, and therapeutic product development. The methods also allow identification of the role of nuclear receptors of unknown functions in cellular homeostaais. Sequences ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that were fused to functional domains and tested for their ability to regulate expression of the ER in living cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New heparanase polynucleotide, useful for controlling disease states such as tumor metastasis, inflammatory diseases and allograft rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; heparanase; cytostatic; vasotropic; antidiabetic; anti-HIV; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; antipsoriatic; antibacentive; neuroprotective; notropic; cerebroprotective; antibacterial; virucide; protozoacide; fungicide; antiinflammatory; cardiant; immunosuppressive; tumour metastasis; inflammatory disease; allograft rejection; cell migration; anglogenesis; basement membrane; extracellular matrix; cancer; ischaemia; diabetic retinopathy; macular degeneration; rheumatoid arthritis; psoriasis; HIV infection; sickle cell anaemia; Alzheimer's disease; macular dystrophy; neurodegenerative disease; vascular disease; candiovascular disease; cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.
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100.0%; Pred. No. 1.7e+06;
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control of disease states such as tumour metastasis, inflammatory diseases, allograft rejection, and for inhibiting processes such as cell migration, angiogenesis, and degradation of the basement membrane and/or extracellular matrix. Heparanase-targeted DNA binding domains modulates gene expression, and are useful for therapeutic or prophylactic applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell anaemia, Alzheimer's disease, unscular dystrophy, neurodegenerative disease, vascular disease, cardiovascular disease, cystic fibrosis, stroke, and bacterial, protozoal, fungal and viral infection. Constructs of the invention may also be useful in gene therapy. The current sequence represents a finger of a three-finger ZFP (zinc finger protein), which has a target site in the human heparanase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; heparanase; cytostatic; vasotropic; antidiabetic; anti-HIV; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; antianaemic; neuroprotective; nootropic; cerebroprotective; cardiant; neuroprotective; nootropic; cerebroprotective; cardiant; immunosupessive; tumour metastasis; inflammatory; cardiant; immunosupessive; tumour metastasis; inflammatory disease; extracellular matrix; cancer; ischaemia; diabetic retinopathy; macular degeneration; rheumatoid arthritis; psoriasis; HIV infection; sickle cell anaemia; Alzheimer's disease; muscular dystrophy; neurodegenerative disease; vascular disease; cardiovascular disease; cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.
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The invention relates to novel heparanase sequences, particularly novel sequences from the regulatory regions upstream and downstream of the coding region. The activity of polynucleotides of the invention may be described as, cytostatic, vasotropic, antidiabetic, anti-HIV, ophthalmological, antirheumatic, antiarthritic, antipsoriatic,

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                                                                         control of disease states such as tumour metastasis, inflammatory diseases, allograft rejection, and for inhibiting processes such as cell migration, angiogenesis, and degradation of the basement membrane and/or extracellular matrix. Heparansec-targeted DNA binding domains modulates gene expression, and are useful for therapeutic or prophylactic applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular degeneration, rheumatoid arthritis, psoriasis, HIV infection, includation and arthritis, psoriasis, HIV infection, sickle cell anaemia, Alzheimer's disease, unscular disease, cardiovascular disease, cystic fibrosis, stroke, and bacterial, protozoal, fungal and viral infection. Constructs of the invention may also be useful in gene therapy. The current sequence represents a finger of a three-finger ZFP (zinc finger protein), which has a target site in the human heparanase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
antianaemic, neuroprotective, nootropic, cerebroprotective, antibacterial, virucide, protozoacide, fungicide, antiinflammatory, cardiant and immunosuppressive. Modulating expression of heparanase gene using constructs of the invention is useful for facilitating targeted
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 7; DB 5; Le 100.0%; Pred. No. 1.7e+06;
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Best Local Similarity luv...
7; Conservative
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Synthetic.
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that it binds to the S3 target subsite, thus designing (1) that binds to a target site. (1) is useful for recognition of triplet target subsites having the mucleotide G in the 5'-most position of the subsite. (1) is useful in studying gene function, and for human therapeutics and plant engineering. (1), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (1) has improved affinity and specificity for their rarget sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP61230 repersent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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Best Local Similarity 100.
Matches 7; Conservative
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3.-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypebtide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (S) target subsite, selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it compared to the S2 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (A aving the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant complete the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of
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engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP48642 standard; peptide; 7 AA.
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RSDHLAR 7
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                                                                                                                                                                                                           Sequence 7 AA;
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gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. AB071213 to AB071214 and ABP48191 to ABP51210 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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                                                                                                                                                                  100.0%; Score 7; 100.0%; Pred. No.
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RSDHLAR 7
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                                                                                                                           Sequence 7 AA;
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) carget site, comprising a first (FI), a second (F2), and a third (F3) carget site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CT) comprising (I); (2) a polynucleotide (III) encoding (I) or (II) is and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it comprises to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (CT) having the nucleotide (III) is useful in therapeutic methods to useful in studying gene function, and for human therapeutic methods to condulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. AB071213 to that it is expression. (I) has improved affinity and specificity for their carget sequences, as well as enhanced biological activity. AB071213 to incomplet the exemplification of the present
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1.7e+06;
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                                                                    100.0%; Score 7;
100.0%; Pred. No.
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                                                                                                         Local Similarity
nes 7; Conserv
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Sequence 7 AA;
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                                                                    Query Match
Best Local 4
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                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP49518
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Sequence 7 AA;

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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) card tinger, ordered FP, F2. F2 from N-terminus to C-terminus, where the crarget site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) encoding (I) or (II) and (II) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it comparising (M) (I) involves selecting the F2 zinc finger such that it binds to the S1 target subsite, and selecting the F3 zinc finger such that it compared to the S3 target subsite, then designing (I) that binds to the S3 target subsite, then designing (I) that binds to the S3 target subsite, then designing (I) that binds to the S3 target subsite, then designing (I) that binds to the S1 target subsite, then designing (I) that binds to the S1 target subsite, then designing (I) that binds to useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. ABG71213 to ABG72214 and ABG72214 and ABG72213 to especial in the expression of the present confidence the present in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                Zinc finger protein; ZFP; DNA binding protein; zinc finger.
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                                                                                                                                                                                                                                                                         Zinc finger protein related peptide motif SEQ ID NO:679.
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 41; 81pp; English
                                                                                                                                                        ABP48621 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2001; 2001WO-US043438.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-500284/53.
                                                     1 RSDHLAR 7
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                                                                                                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                    28-AUG-2002
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                                                                                                                                                                                               ABP48621;
                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) and zinc finger, ordered F1. F2. F3 from N-terminus to C-terminus, where the carget site comprises, in 3.5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (S1) designing (I); (1) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S1 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites (C1) a target subsite, thus designing (I) that binds to useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to compliance specific detection of target nucleic acid diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity, AB071213 to AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc invarient continuation in the exemplification of the present
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                       Zinc finger protein related peptide motif SEQ ID NO:2545.
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                DB 5; Length 7;
1.7e+06;
                                                       0; Indels
                                                         0; Mismatches
                  Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 54; 81pp; English.
                                                                                                                                                                                                                                    ABP49797 standard; peptide; 7 AA.
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                  100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                (first entry)
Query Match
Best Local Similarity 100.
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                                                                                                1 RSDHLAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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Gaps

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ABP49260;

RESULT 12 ABP49260

30-MAY-2002

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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) and carget site, comprising a first (FI), a second (F2), and a third (F3) and a third (F3) target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (CI) comprising (I); (2) a polymucleotide (III) encoding (I) or (III); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, and selecting the F2 zinc finger such that it comprising (M) (I) involves selecting the F2 zinc finger such that it compared to the S2 target subsite, and selecting the F2 zinc finger such that it compared to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to a target side (I) the S'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutic and plant companies the expression of a target region within a subject, in changed for sequence specific detection of target nucleic acid in sample, and in assays to determined the phenotype and function of the subsiter of target sequences, as well as enhanced biological activity, AB071213 to their comparion to peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                Zinc finger protein; ZFP; DNA binding protein; zinc finger.
                                                                                                                        Zinc finger protein related peptide motif SEQ ID NO:2640.
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100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2001; 2001WO-US043438
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                                                                           28-AUG-2002 (first entry)
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                           ABP50082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu Q;
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ABP48649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target site, comprising a first (F1), a second (F2), and a third (F3) carget site, comprising a first (F1), a second (F2), and a third (F3) carget site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (T1) comprising (I); (2) a polymucleotide (I11) encoding (I) or (I1); and third (S3) target subsite, selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to the S2 target subsite, thus designing (I) that binds to the tracet site. (I) is useful for recognition of triplet target such that it binds to the S3 target subsite, thus designing (I) that binds to useful in studying gene function, and for human therapeutics and plant custum the tudying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in charget sequence specific detection of target nucleic acid diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced biological activity. AB071213 to the AB072214 and AB0848191 to AB051230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes a zinc finger protein (I) that binds to a
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                                                                                                                                                                                                                                                                                               Zinc finger protein; ZFP; DNA binding protein; zinc finger
                                                                                                                                                                                                                                          Zinc finger protein related peptide motif SEQ ID NO:1388.
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                                                                                 ABP49260 standard; peptide; 7 AA
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Best Local Similarity 100.
Matches 7; Conservative
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Synthetic.
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Gaps

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28-AUG-2002 (first entry)

ABP50082 ID ABP50082 standard; peptide; 7 AA.

RESULT 13

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Length 7;

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New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
                                                                                                                                                                                         (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                         20-NOV-2000; 2000US-00716637.
                                                                                                                           20-NOV-2001; 2001WO-US043438
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                                                            WO200242459-A2
             ношо варіепв
                                                                                           30-MAY-2002
                              Synthetic.
                                                                                                                                                                                                                        Liu Q;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) target site, comprising a first (F1), a second (F2), and a third (F3) target site comprises, in 3'-5' direction, a first (G1), a second (S2), and a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polymuclectide (III) encoding (I) or (II); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S1 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, and selecting of F3 zinc finger such that it binds to the S3 target subsite, in description of triplet target subsites a target site. (I) is useful for recognition of triplet target subsites a target site. (I) is useful for recognition of the subsite. (I) is useful in studying gene function, and for human therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of the sample, and in assays to determined the phenotype and function of target sequences, as well as enhanced alfinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABB74230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                    New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.
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                                             Zinc finger protein; ZFP; DNA binding protein; zinc finger.
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             Zinc finger protein related peptide motif SEQ ID NO:893.
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 41; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP49794 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                        (SANG-) SANGAMO BIOSCIENCES INC
                                                                                                                                                                                                                        20-NOV-2000; 2000US-00716637.
                                                                                                                                                                                         20-NOV-2001; 2001WO-US043438,
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                                                                                                                                                                                                                                                                                                                       WPI; 2002-500284/53.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                           WO200242459-A2.
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                                                                              sapiens
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                                                                                                                                                           30-MAY-2002.
                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                        Liu Q;
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The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (FI), a second (F2), and a third (F3) and cardered F1, F2, F3 from N-terminus to C-terminus, where the card a third (S3) target subsite. Also described are: (I) a polypeptide (II) comprising (I); (2) a polyhucleotide (III) encoding (I) or (III); and (II) designing (I); (2) a polyhucleotide (III) encoding (I) or (III); and (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it comparison (I) is useful for recognition of triplet target subsites that it binds to the S3 target subsite, thus designing (I) that binds to the S1 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the S3 target subsite, thus designing (I) that binds to the tit binds to the S3 target subsite, thus designing (I) that binds to useful in studying gene function, and for human therapeutic subsites (I) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determined the phenotype and function of the subsites. (I) as suppression (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity, AB071213 to their finger peptides which are given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 7; DB 5; Le 100.0%; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Example 1; Page 54; 81pp; English
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSDHLAR 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 27, 2004, 21:40:45; Search time 20 Seconds (without alignments) 23.211 Million cell updates/sec

US-09-846-033B-252

1 TKDHLVR 7 Title: Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

478139 seqs, 66318000 residues Searched:

7

Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

1: /cgr2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB

Description

No matches found

Search completed: December 27, 2004, 22:06:56 Job time : 20.1667 secs

```
GenCore version 5.1.6
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```

OM protein - protein search, using sw model

December 27, 2004, 21:40:45; Search time 20 Seconds (without alignments) 23.211 Million cell updates/sec Run on:

US-09-846-033B-251 Title: Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 1 TTGHLVR 7 Scoring table: Sequence:

478139 segs, 66318000 residues Searched:

7 Word size :

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description H Query Score Match Length DB Result No.

No matches found

Search completed: December 27, 2004, 22:06:56 Job time: 20.1667 BecB

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

December 27, 2004, 21:40:45 ; Search time 20 Seconds (without alignments) 23.211 Million cell updates/sec

US-09-846-033B-250

1 TAGHLVR 7 Title: Perfect score: Scoring table: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0

478139 segs, 66318000 residues Searched:

7

Total number of hits satisfying chosen parameters: Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Issued_Patents_AA:* Database

1: /cgn2 6/ptcdata1/laa/5A COMB.pep:*
2. /cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description 10 Query Score Match Length DB Result No.

No matches found

Search completed: December 27, 2004, 22:06:56 Job time: 20.1667 secs

us-09-846-033b-249.olig7.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 27, 2004, 21:40:45 ; Search time 20 Seconds (without alignments) 23.211 Million cell updates/sec Run on:

US-09-846-033B-249 7 1 TSGHLRR 7 Title: Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0

Scoring table:

478139 segs, 66318000 residues Searched:

7 Word size : Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database

lssued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Ω Query Score Match Length DB Š. Result

No matches found

Search completed: December 27, 2004, 22:06:56 Job time : 20.1667 secs

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Gaps

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Length 136;

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APPLICANT:
APPLICANTION:
AUTHER OF INVENTION:
AUTHER OF INVENTION:
APPLICATION NUMBER:
APPLICA
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100.0%; Score 7; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 7; Conservative 0; Mismatches 0. Thath
                                                                        100.0%; Score 7; DB 4; 100.0%; Pred. No. 0.36;
                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 27, 2004, 22:06:56 Job time: 20.1667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7709, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Klebsiella pneumoniae US-09-489-039A-7709
                                                                            Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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US-09-248-796A-19633
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US-09-489-039A-7709
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Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19633
LENGTH: 136
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Sequence 7709, Ap
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                                                                                                                                                                                                                                                                            December 27, 2004, 21:40:45; Search time 20 Seconds (without alignments) 23.211 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgm2_6/prodata/1/iaa/5A_COMB.pep:*
/cgm2_6/prodata/1/iaa/5B_COMB.pep:*
/cgm2_6/prodata/1/iaa/6A_COMB.pep:*
/cgm2_6/prodata/1/iaa/6A_COMB.pep:*
/cgm2_6/prodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/prodata/1/iaa/PCTUS_COMB.pep:*
                                                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-248-796A-19633
US-09-489-039A-7709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478139 segs, 66318000 residues
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                                                                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-846-033B-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Score Match Length DB
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ORGANISM: Candida albicans
                                                                                        Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TSGHLAR 7
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
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Gaps

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OM protein - protein search, using sw model

December 27, 2004, 21:40:45; Search time 20 Seconds (without alignments) 23.211 Million cell updates/sec Run on:

US-09-846-033B-247 Title: Perfect score: Sequence:

1 TSGHLSR 7

OLIGO Gapóp 60.0 , Gapext 60.0 Scoring table:

478139 seqs, 66318000 residues Searched:

7 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2 6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2 6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2 6/ptodata/1/laa/5A_COMB.pep:*

4: /cgn2 6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*

6: /cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü Query Score Match Length DB Result No.

Description

No matches found

Search completed: December 27, 2004, 22:06:56 Job time : 20.1667 secs

us-09-846-033b-108.olig7.rai

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec Run on:

US-09-846-033B-108 1 RSDALTQ 7 Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched:

478139 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 7 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

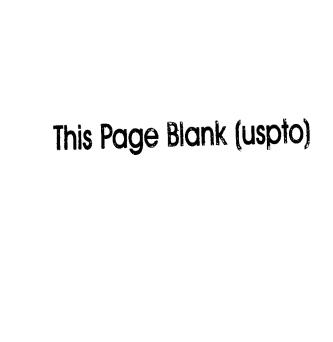
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description H Query Score Match Length DB No. Result

Search completed: December 27, 2004, 21:40:39 Job time : 16.35 secs

No matches found



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec

US-09-846-033B-107 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 1 QSGNLTR 7 Scoring table:

478139 segs, 66318000 residues Searched:

7 Word size : Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by ohance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü Query Score Match Length DB Result No.

Description

No matches found

Search completed: December 27, 2004, 21:40:39 Job time : 16.35 secs

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Scoring table:

Word size :

Database

Searched:

Perfect score:

Sequence:

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CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-716-637-29
; Sequence 29, Application US/09716637
; Patent No. 6794136
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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US-09-779-233-44
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LENGTH: 7
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LENGTH: 7
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Sequence 14, Application US/09731558
Patent NO. 6503717
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Sangame Blosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-0003210US
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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28.393 Million cell updates/sec
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Sequence 30, 2
Sequence 18, 2
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Sequence 29,
Sequence 15,
Sequence 15,
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                                                                                                                                                December 27, 2004, 20:31:09 ; Search time 16.35 Seconds
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2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-44
US-09-229-037-15
US-09-478-681-15
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-779-233-18
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                                                                                                          OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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APPLICANT: EISENBERG, Stephen P.
APPLICANT: LIU Qiang
APPLICANT: LIU Qiang
APPLICANT: LIU Qiang
APPLICANT: REBAR, Edward
TITLE OF INVENTION: TERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DAFE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix US-09-779-233-44
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CTHER INFORMATION: Description of Artificial Sequence:SBS3; OTHER INFORMATION: recognition helix US-09-731-558-14
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Fatent No. 668958
GENERAL INFORMATION:
APPLICANT: Case, Case, TILE OF INVENTION:
CURRENT APPLICATION UNBER: US/09/779,233
CURRENT PILIG DATE: 201-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
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US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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APPLICANT: Case, Casey Christopher
APPLICANT: Bisenbarg, Stephen P.
APPLICANT: Branbarg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Segulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 10999-6.002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE Patentin Ver. 2.0
SEQ ID NO 15
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Sequence 15, Application US/09478681

Sequence 15, Application US/09478681

Sequence 15, Application US/09478681

Sequence 15, Application US/09478681

Sequence 15, Application US 0607882

APPLICANT: Case, Casey Christopher

APPLICANT: Eisenberg, Stephen P.

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REQUIATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZING FINGER PROTEINS

FILE REFERENCE: 8325-0002.10 / S2-US3

CURRENT FILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
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                                                                                       100.0%; Score 7; DB 4; Length 7; ilarity 100.0%; Pred. No. 3.8e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             US-09-229-037-15
Sequence 15, Application US/09229037A
Patent No. 6534261
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 99
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Solventian Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
TITLE OF INVENTION: 2inc Finger Proteins
TITLE OF INVENTION: 1099-01-12
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
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; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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                                                                                                                    Length 99;
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; Sequence 3, Application US/09779233
; Sequence 3, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
; APPLICAMY: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REPREBRENCE: 8232-0010
; CURRENT APPLICATION UNMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
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0.16;
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US-09-478-681-30
Sequence 30, Application US/09478681
Fatent No. 6607882
GENERAL INFORMATION:
APPLICANT: Cox III, George N.
APPLICANT: Case, Casey Christopher
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINNER PROTEINS
FILE REFERENCE: 3050-002.10 / S2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 30
LENGTH: 196
LENGTH: 196
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; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF 3a/1
US-09-779-233-18
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233

Patent No. 6689558

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REFERENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ 1D NOS: 45

SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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178 RSDHLSR 184
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Indela Length 7;

Scoring table:

Word size :

Database

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Perfect score:

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Sequence:

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APPLICANT: EISTREEG, Stephen P.
APPLICANT: EISTREEG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: TAMESON, Andrew
APPLICANT: REBAR, Edward
TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT PILLING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SSC ID NO 29
LENGTH: 7
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                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7; DB 4; Length 100.0%; Pred. No. 3.8e+05;
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ilarity 100.0%; Pred. No. 3.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION UNMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
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PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR PILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09716637
Patent No. 6794136
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 44, Application US/09779233; Patent No. 6689558; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
7; Conserve
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Matches 7; Conserv
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RSDHLSR 7
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US-09-779-233-44
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LENGTH: 7
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APPLICANT: Rebar, Edward J.
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Processing for the Identification of Gene Function
FILE REFERENCE: 019496-00321008
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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28.393 Million cell updates/sec
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Sequence 30,
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Sequence 18,
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                                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-44
US-09-229-037-15
US-09-478-681-15
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-779-233-18
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Gapop 60.0 , Gapext 60.0
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Patent No. 6503717
GENERAL INFORMATION
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
                                                                                                                                                                                                                                                                             US-09-846-033B-105
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Maximum DB seq length: 200000000
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Match Length DB
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Ease, Casey Christopher
APPLICANT: Essenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-0022000S
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
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OTHER INFORMATION: construct targeting upstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
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US-09-779-233-3
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                                                                                                    Length 99;
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                                                                                                    100.0%; Score 7; DB 4;
100.0%; Pred. No. 0.16;
ive 0; Mismatches
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; Sequence 3, Application US/09779233
; Sequence 3, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
; APPLICANT: Case, Case,
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; TITLE OF INVENTION UNMER: US/09/779,233
; CURRENT APPLICATION NUMBER: US/09/779,233
; UNMER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 196
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Best Local Similarity
Matches 7; Conserv
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                                  ; OTHER INFORM
US-09-478-681-15
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APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Jarvis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Songamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
SUTMER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6607882

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZINC FINGER PROTEINS

FILE REFERENCE: 8325-0002.10 / S2-US3

CURRENT APPLICATION NUMBER: US/09/478, 681

CURRENT PILING DATE: 2000-01-06

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
                          ), OTHER INFORMATION: Description of Artificial Sequence: VEGF-I US-09-716-637-29
                                                                                  100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.88+05; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                             US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
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                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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US-09-478-681-15
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LENGTH: 99
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LENGTH: 99
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US-09-478-681-30
Squence 30, Application US/09478681
Fatent No. 6607882
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Elsenberg, Stephen P.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FURGR PROTEINS
TITLE OF INVENTION: USING ZINC FURGR PROTEINS
TITLE OF INVENTION UNMBER: US/09/478,681
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENT IS6
LENGTH: 196
LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
FEBRIURE:
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US-09-779-233-18
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233

Sequence 18, Application US/09779233

GENERAL INFORMATION:

TITLE OF INVENTION: Casey

TITLE OF INVENTION: Calls FOR DRUG DISCOVERY

FILE REFERENCE: 8325-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PAT 196

TENGTH: 196

TENGTH: 196

TORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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178 RSDHLSR 184
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1 RSDHLSR 7
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Search completed: December 27, 2004, 21:40:38 Job time : 16.35 secs

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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

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Database :

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APPLICANT: EISENBERG, Stephen P.
APPLICANT: EISENBERG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
APPLICANT: EISENBERG, Andrew
APPLICANT: BEBAR, Edward
TITLE OF INVENTION: TERRATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: recognition
OTHER INFORMATION: helix
US-09-779-233-44
                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 44, Application US/09779233
; Patent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION:
; FILE REPRENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 44
            PRIOR APPLICATION NUMBER: US 09/456,100 PRIOR FILING DATE: 1999-12-06 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; sequence 29, Application US/09716637; Patent No. 6794136; GENERAL INFORMATION:
CURRENT FILING DATE: 2000-12-06
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-779-233-44
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Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 30, Appl
Sequence 18, Appl
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APPLICANT: Case, Casey Christopher

APPLICANT: Case, Casey Christopher

APPLICANT: Liu, Qiang

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

APPLICANT: Sangamo Biosciences, Inc.

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019456-001210US

CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec
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Sequence 44
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-719-233-44
US-09-716-637-29
US-09-229-037-15
US-09-779-233-3
US-09-478-681-30
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                                                                                                                         OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                            US-09-846-033B-104
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Maximum DB seq length: 200000000
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Result No.

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; Sequence 30, Application US/09229037A; Patent No. 6534261
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Best Local Similarity luv...
7; Conservative
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Matches 7; Conservative
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81 RSDHLSR 87
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US-09-229-037-30
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Patent No. 6607882

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Case, Casey Christopher

APPLICANT: Elsenberg, Stephen P.

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REGULATION OF ENDOCENOUS GENE EXPRESSION IN CELLS

TITLE OP INVENTION: USING ZINC FINGER PROTEINS

TILLE APPLICANT: 3125-0002.10 / S2-US3

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT FILING DATE: 2.00-01-06

NUMBER OF SEQ ID NOS: 43
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 ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
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                                                               100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                US-09-229-037-15
; Sequence 15, Application US/09229037A
; Petent No. 6534261
; GENERAL INFORMATION:
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                                                   Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-478-681-15
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LENGTH: 99
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GENERAL INFORMATION:
APPLICANT: Cas (II), George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Sisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Spratt, Sharon Kaye
TITLE OF INVENTION: Requiation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
TITLE OF INVENTION: Suc 1999-602200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 30
LENGTH: 196
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; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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100.0%; Pred. No. 0.16;
rative 0; Mismatches
                                                                                            100.0%; Score 7; DB 4; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                        RESULT 6

8.09-779-233-3

Sequence 3, Application US/09779233

Patent No. 668958

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

TITLE OF INVENTION: CASE, CASEY

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 3

LENGTH: 99
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US-09-478-681-30
IS Sequence 30, Application US/09478681
Fatent No. 6607882
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Spratt, Sharon K.
APPLICANT: Spratt, Sharon K.
APPLICANT: Spratt, Sharon K.
APPLICANT: Spratt, Sharon K.
APPLICANT: USING ZINC FINGER PROTEINS
FILE REFRENCE: 8125-0002.10 / S2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT PILING DATE: 2000-01-06
NUMBER OP SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 30
LENGTH: 196
LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
FRAT
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US-09-779-233-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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US-09-779-233-18
Sequence 18, Application US/09779233
Fatent No. 6689558
GENERAL INFORMATION:
APPLICANT: Case, Casey,
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY;
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT APLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 18
LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
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178 RSDHLSR 184
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Title: Perfect score:

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Sequence:

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Sequence 29, Application US/09716637

Sequence 29, Application US/09716637

Sequence No. 6794136

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: LIV. Qiang

APPLICANT: TEBAR, Edward

TITLE OF INVENTION: IPERATIVE OPTIMIZATION IN THE DESIGN OF BINDING

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTION: PROTEINS

CURRENT APPLICATION NUMBER: US/09/716,637

CURRENT APPLICATION NUMBER: US/09/716,637

CURRENT PILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix
                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44, Application US/09779233
Fatent No. 6689558
GENERAL INFORMATION:
APPLICANT: Gase, Casey
TITLE OF INVENTION:
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOCTHWARE: Patentin Ver. 2.0
SEQ ID NO 44
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                   NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 7
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Best Local Similarity 100...
7, Conservative
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Best Local Similarity
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1 RSDHLSR 7
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US-09-779-233-44
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Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 30, Appl
Sequence 18, Appl
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APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                  December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec
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Sequence 44,
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1: /cgn2_6/ptodaca1/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodaca1/iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-44
US-09-229-037-15
US-09-779-233-3
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US-09-779-233-18
US-09-779-233-18
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Patent No. 6503117
GENERAL INFORMATION
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
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Maximum DB seq length: 200000000
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| General AUC. DD334201 |
| General AUC. DD334201 |
| APPLICANT: Case, Casey Christopher |
| APPLICANT: Case, Casey Christopher |
| APPLICANT: Case, Casey Christopher |
| APPLICANT: Bisenherg, Stephen P. |
| APPLICANT: Barvis, Eric Edward |
| APPLICANT: Spratt, Sharon Kaye |
| APPLICANT: Sargame Bisosfiences, Inc. |
| APPLICANT: Sargame Bisosfiences, Inc. |
| TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using |
| TITLE OF INVENTION: Zinc Finger Proteins |
| TITLE OF INVENTION: Zinc Finger Proteins |
| TITLE OF STORE APPLICATION NUMBER: US/09/229, 037A |
| CURRENT APPLICATION NUMBER: US/09/229, 037A |
| NUMBER OF SEQ ID NOS: 40 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 30 |
| LENGTH: 196
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  ; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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                                                                                                           Length 99;
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                                                                                             100.0%; Score 7; DB 4; illarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09779233
; Sequence 3, Application US/09779233
; Fatent No. 6689558
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT PILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 30, Application US/09229037A; Patent No. 6534261
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Best Local Similarity
Matches 7; Conservat
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Elsenberg; Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Songamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
SUPRENT FILING DATE: 1999-01-12
SUBMER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VET. 2.0
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Javvis, Eric E.
APPLICANT: Spratt, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REPERENCE: 8325-0002.10 / S2-US3
CURRENT APPLICATION NUMBER: US/09/478,681
CURRENT APPLICATION NUMBER: US/09/478,681
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: VEGF1 ZFP OTHER INFORMATION: construct targeting upstream 9-base pair target is OTHER INFORMATION: site in VEGF promoter US-09-229-037-15
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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                                                                                                              Query Match 100.0%; Score 7; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  US-09-229-037-15
; Sequence 15, Application US/09229037A
; Patent No. 6534261
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/09478681 Patent No. 6607882 GENERAL INFORMATION: APPLICANT: Cox III, George N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-478-681-15
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LENGTH: 99
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LENGTH: 99
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                                                                                                                                            Sequence 30, Application US/09478681

Sequence 30, Application US/09478681

Patent No. 6607882

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Eisenberg, Stephen P.

APPLICANT: Spratt, Sharon K.

APPLICANT: Spratt, Sharon K.

TITLE OF INVENTION: REGILATION OF ENDOCENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZINC FINGER PROTEINS

TITLE OF INVENTION: USING ZINC FINGER

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT PAPPLICATION NUMBER: US/09/478,681

CURRENT PAPPLICANTON NUMBER: US/09/478,681

CURRENT PAPPLICANTON NUMBER: US/09/478,681

CURRENT PAPPLICANTON NUMBER: US/09/478,681

CURRENT PAPPLICANTON NUMBER: US/09/478,681
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US-09-779-233-18
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100.0%; Score 7; DB 4; Length 196;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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US-09-779-233-18
Sequence 18, Application US/09779233
Patent No. 668958
GENERAL INFORMATION:
APPLICANT: Case, Casey
TILE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT APPLICATION NUMBER: 201-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
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178 RSDHLSR 184
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1 RSDHLSR 7
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Scoring table:

Sequence:

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Searched:

Database :

Result No.

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Sequence 29, Application US/09716637

Sequence 29, Application US/09716637

Sequence No. 6794136

GENERAL INFORMATION:

APPLICANT: EISENBERG, Stephen P.

APPLICANT: LIU, Olang

APPLICANT: AMMIESON, Andrew

APPLICANT: REBAR, Edward

TITLE OF INVENTION: IPRATIVE OPTIMIZATION IN THE DESIGN OF BINDING

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: 8325-0020

CURRENT PELING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 35

SOTTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: recognition ; OTHER INFORMATION: helix
US-09-779-233-44
                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Fatent No. 668958
GENERAL INFORMATION:
APPLICANT: Case, Case,
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT PAPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOGTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 7
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           PRIOR APPLICATION NUMBER: US 09/456,100 PRIOR FILING DATE: 1999-12-06 NUMBER OF SEQ ID NOS: 24 SEC ID NO 14 LENGTH: 7
CURRENT FILING DATE: 2000-12-06
                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 7; Conservative
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US-09-779-233-44
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Sequence 29, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 18, Appli
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Patent No. 650371.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proceins for the Identification of Gene Function
FILE REPERENCE: 0190496-00321008
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-779-233-49
US-09-229-037-15
US-09-478-681-15
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-779-233-18
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                                                                                                                                                                December 27, 2004, 20:31:09
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                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Gaps

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Endogenous Gene Expression in Cells Using
OTHER INFORMATION: construct targeting upstream 9-base pair target OTHER INFORMATION: site in VEGF promoter
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US-09-779-233-3
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100.0%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches
                                                                                                  100.0%; Score 7; DB 4; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                               US-09-179-233-3
; Sequence 3, Application US/09779233
; Sequence 3, Application US/09779233
; Faterix No. 668558;
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; TILE REFERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779,233
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 99
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GRERAL INFORMATION:
APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Sprate, Sharon Kaye
APPLICANT: Sprate, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous (
TITLE OF INVENTION: Regulation of Endogenous (
TITLE OF INVENTION: 2inc Finger Proteins
TITLE OF INVENTION: 2inc Finger Proteins
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILIAG DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH 106
                                                                                                                                                    0; Mismatches
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; Sequence 30, Application US/09229037A
; Patent No. 6534261
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RSDHLSR 87
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                                                 US-09-478-681-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Stsenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Sarat, Sharon Kaye
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
TITLE OF INVENTION: Zinc Finger Proteins
FILE REFERENCE: 019496-002200US
FURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Gracherg, Stephen P.
APPLICANT: Spract, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
FILE REFERENCE: 8325-0002.10 / S2-US3
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 99
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                            ; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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                                                                                                  Query Match 100.0%; Score 7; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 15, Application US/09229037A

; Patent No. 6534261

; GENERAL INFORMATION:
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; Sequence 15, Application US/09478681
; Patent No. 6607882
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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LENGTH: 99
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| Sequence 30, Application US/09478681
| Patent No. 6607882
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Case, Casey Christopher
| APPLICANT: Elsenberg, Stephen P. APPLICANT: Elsenberg, Stephen P. APPLICANT: Estenberg, Stephen P. APPLICANT: By APPLICANT: Spratt, Sharon K. TITLE OF INVENTION: REGILATION OF ENDOGENOUS GENE EXPRESSION IN CELLS TITLE OF INVENTION: USING ZINC FINGER PROTEINS
| TITLE OF INVENTION: USING ZINC FINGER PROTEINS
| FILE REFERENCE: 8325-0002.10 / S2-US3 | CURRENT APPLICATION NUMBER: US/09/478,681 |
| CURRENT APPLICANT: 2000-01-06 | SCOFTWARE: Patentin Ver. 2.0 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 30 |
| TYPE: PRT |
| CORGANISM: Artificial Sequence |
| CONTING AND APPLICANT: SEQUENCE |
| CONTING AND APPLICANT |
| CONTI
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US-09-779-233-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233
Sequence 18, Application US/09779233
Sequence 18, Application US/09779233
GENERAL INPORMATION:
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFRENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT APPLICATION NUMBER: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 18
LENGTH: 196
TYPE: PRT
ORGANISM: Artificial Sequence
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178 RSDHLSR 184
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Search completed: December 27, 2004, 21:40:38 Job time : 16.35 secs

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US2003021776-A1
WO200246412-A2
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                    13-JUN-2002
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Jarvis E;
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Jarvis E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zinc finger protein; angiogenesis; vasculogenesis; ischaemia; diabetic retinopathy; psoriasis; arthropathy; cancer; tumour growth; gene therapy; antiatherosclerotic; vasotropic; antiarthritic; vulnerary; antitleer; cytostatic; antipsoriatic; antidiabetic; ophthalmological; osteopathic; antiinfertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abj03961 Human VEG
Abo14621 Human VEG
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                                                                           December 27, 2004, 20:25:55 ; Search time 64.3 Seconds (without alignments) 39.053 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human VEGF-targeted zinc finger protein fragment SEQ ID NO: 246
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     2002273 segs, 358729299 residues
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                                                       OM protein - protein search, using sw model
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ABO14621
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Perfect score:
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No.
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Zinc finger protein; vascular endothelial growth factor; VEGF; ischaemia; atherosclerosis; tumour; arthritis; bone injury; wound; ulcer; surgery; angiogenesis; pregnancy; embryogenesis; human; recognition helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger protein that binds to target site in vascular endothelial growth factor gene, useful for modulating expression of the gene and for treating atherosclerosis, ischemia, arthritis, wound or ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a zinc finger protein that binds to a target site in one or more vascular endothelial growth factor (VEGF) genes. The protein is useful for modulating expression of a VEGF gene, thereby regulating angiogenesis and vasculogenesis. This can be used to treat atherosclerosis, ischaemia, arthritis, wounds, ulcers, tumours, diabetic retinopathy or psoriasis. The present sequence is a peptide shown in the invention
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                                                                                                                                                                                                                                                                       Jamieson A, Liu Q, Liu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jamieson A, Liu Q, Liu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 103; 195pp; English.
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                                                                                                                                                                                                      (SANG-) SANGAMO BIOSCIENCES INC.
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12-DEC-2000; 2000US-00736083.
30-APR-2001; 2001US-00846033.
                                                                                                 12-DEC-2000; 2000US-00736083.
30-APR-2001; 2001US-00846033.
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06-DEC-2001; 2001WO-US046861
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Best Local Similarity 100.
Matches 7; Conservative
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WPI; 2003-466074/44.
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The invention relates to a zinc finger protein that binds to a target site. The zinc finger protein is useful for modulating expression of a vascular endothelial growth factor (VEGF) gene. The expression of a number of splice variants of 'VEGF gene is modulated. A number of target is sites are contacted with a number of zinc finger proteins and each zinc finger protein binds to a distinct target site. The zinc finger protein is administered in combination with a delivery vehicle, or its nucleic acid is administered into the cell, either in naked form or delivered in a expression vector. The zinc finger protein or nucleic acid is useful for treating a disease or injury such as atherosclerosis, ischaemia, tumour, arthritis, bone injury such as atherosclerosis, ischaemia, tumour, arthritis, bone injury wounds and ulcer in a subject. The zinc finger protein is also useful for modulating angiogenesis, by introducing the zinc finger protein into an animal, where the animal has a genome comprising a target site within a WEGF gene. The zinc finger protein and nucleic acid are also useful for creening for a modulator of expression of a VEGF gene. The zinc finger protein and nucleic acid are also useful for compus luteum and endometrium, which is useful for intilating and/or maintaining pregnancy and for supporting embryogenesis. The zinc finger protein and its nucleic acid are also useful in surgical applications. The present sequence represents the amino acid sequence of a human VEGF targeted zinc finger protein ZFP recognition helix
                                                        Novel zinc finger protein that binds to a target site, useful for modulating vascular endothelial growth factor gene expression, for modulating angiogenesis, for wound healing and for treating ischemia.
                                                                                                                                                                                      Disclosure, Page 43; 120pp; English.
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Sequence 7 AA;

Gaps . 0 0; Indels Query Match 100.0%; Score 7; DB 6; Length 7; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 7; Conservative 0; Mismatches 0; Indels

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Search completed: December 27, 2004, 21:35:10 Job time : 64.3 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec

US-09-846-033B-246 7 1 TSGHLIR 7 Title: Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

478139 seqs, 66318000 residues Searched:

7 Word size

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

lssued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description ü Query Score Match Length DB Result

No matches found

Search completed: December 27, 2004, 21:40:40 Job time : 16.35 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 27, 2004, 20:31:09; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec Run on:

US-09-846-033B-245 Title: Perfect score:

OLIGO Gapop 60.0 , Gapext 60.0 1 TSGHLTR 7 Scoring table: Sequence:

478139 segs, 66318000 residues Searched:

^ Word size : Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Issued_Patents_AA:* Database :

1: /cgn2 6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/5B COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü Query Score Match Length DB Result No.

Description

No matches found

Search completed: December 27, 2004, 21:40:40 Job time : 16.35 secs

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Search completed: December 27, 2004, 21:40:40 Job time : 16.35 secs
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Sequence 17, Application US/09731558

Patent No. 6503717

GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher

APPLICANT: Expandance of Casey Christopher

APPLICANT: Bangamo Biosciences, Inc.

TITLE OF INVENTION: Proteins for the Identification of Gene Function

TITLE OF INVENTION: Proteins for the Identification of Gene Function

FILE REFERENCE: 019496-003210US

CURRENT APPLICATION NUMBER: US/09/731,558

CURRENT FILING DATE: 2000-12-06

PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 17

LENGTH: 7
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Sequence 37, Appl
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28.393 Million cell updates/sec
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2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-37
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Maximum DB seq length: 200000000
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US-09-731-558-17
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; TYPE: PRT;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SBS6
; OTHER INFORMATION: recognition helix
US-09-731-558-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                               100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        RESULT 2
US-09-779-233-37

Sequence 37, Application US/09779233

Patent No. 6689588

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION:

FILE REPERENCE: 8125-0010

CURRENT APPLICATION NUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                         Conservative
                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conserv
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Gaps

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Length 7; 0; Indels

Scoring table:

Word size :

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Searched:

Perfect score:

Run on:

Sequence:

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Sequence 29, Application US/09716637

Sequence 29, Application US/09716637

Sequence No. 6794136

GENERAL INFORMATION:
APPLICANT: EISENBERG, Stephen P.
APPLICANT: LIU, Qiang
APPLICANT: REBAR, Edward
APPLICANT: REBAR, Edward
TITLE OF INVENTION: ITERATIVE OPTIMIZATION IN THE DESIGN OF BINDING
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT APPLICANTION NUMBER: US/09/716,637
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE PATEUT NUMBER: 200-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix
                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44, Application US/09779233
Sequence 44, Application US/09779233
Patent No. 6689558
GENERAL INFORMATION:
APPLICANT: Case, Casey, TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY; FILE REFERENCE: 8125-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT PILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 14
LENGTH: 7
                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
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1 RSDHLSR
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US-09-779-233-44
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LENGTH: 7
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Sequence 29, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 10, Appli
Sequence 10, Appli
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Patent No. 650371.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
APPLICANT: Sangawo Bisosiences, Inc.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proceins for the Identification of Gene Function
FILE REPERENCE: 019496-003210105
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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28.393 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-716-637-29
US-09-229-037-15
US-09-779-233-3
US-09-478-681-30
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                                                                                                                          OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Gaps

Gaps

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Length 99; 0; Indels

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GENERAL INCORDATES.

APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Cox III, George No. 6534261bert
APPLICANT: Case, Casey Christopher
APPLICANT: Bisenberg, Stephen P.
APPLICANT: Bisenberg, Eric Edward
APPLICANT: Sangamo Biosciences, Inc.
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Zinc Finger Proteins
TITLE OF INVENTION: Zinc Finger Proteins
FILE REPERENCE: 019496-002200US
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 7; DB 4; Length 196; Best Local Similarity 100.0%; Pred. No. 0.3; Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches
                                                                                                 100.0%; Score 7; DB 4;
100.0%; Pred. No. 0.16;
tive 0; Mismatches
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; Sequence 3, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
; APPLICAMT: Case, Casey
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REPERENCE: 8325-0010
; CURRENT APPLICATION UNMBER: US/09/779,233
; CURRENT PILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-229-037-30
; Sequence 30, Application US/09229037A
; Patent No. 6534261
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Best Local Similarity
7; Conserva
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APPLICANT: Case, Casey Christopher
APPLICANT: Case, Elsenberg, Stephen P.
APPLICANT: Jarvis, Eric Edward
APPLICANT: Jarvis, Eric Edward
APPLICANT: Spratt, Sharon Kaye
APPLICANT: Songamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
FILE REFERENCE: 019496-002200US
CURRENT APPLICATION NUMBER: US/09/229,037A
CURRENT PILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Case, Casey Christopher
APPLICANT: Bracherg, Stephen P.
APPLICANT: Spract, Sharon K.
TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
TITLE OF INVENTION: USING ZINC FINGER PROTEINS
CURRENT PRILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 99
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    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I
US-09-716-637-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 7; DB 4; Length 99; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Indels
                                                                                                                                                   0; Indels
                                                                                                      Length 7;
                                                                                                   100.0%; Score 7; DB 4; L 100.0%; Pred. No. 3.8e+05;
                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09478681
Patent No. 6607882
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Best Local Similarity 100.
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Best Local Similarity 100
Matches 7; Conservative
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US-09-478-681-15
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Length 99; 0; Indels ö

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RESULT 8

US-09-478-681-30

i Sequence 30, Application US/09478681

patent No. 6607882

GENERAL INFORMATION:

APPLICANT: Cax III, George N.

APPLICANT: Case, Casey Christopher

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

APPLICANT: Bisenberg, Stephen P.

TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS

TITLE OF INVENTION: USING ZINC PINGER PROTEINS

TITLE OF INVENTION: USING ZINC PINGER PROTEINS

TILLE REFERENCE: 8325-0002.10 / 32-U33

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT APPLICATION NUMBER: US/09/478,681

CURRENT APPLICATION OFTE: 2000-01-06

NUMBER OF SEQ ID NOS: 43

CENTRAIN FILL NOS: 43

CORRIENT PRING DATE: 2000-01-06

SOFTWARE: PATENTING DATE: 2000-01-06

TYPE: PRT

CORRIENT PRING DATE: 2000-01-06

SOFTWARE: PATENTING DA
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US-09-779-233-18
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233
Sequence 18, Application US/09779233
Sequence 18, Application US/09779233
GENERAL INFORMATION:
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING NOS: 45
SOFTWARE: PAT CALLIFICIAL Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: December 27, 2004, 21:40:40 Job time : 16.35 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||||||
178 RSDHLSR 184
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Length 7;

Scoring table:

Word size :

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Result No.

Searched:

Perfect score:

Title:

Run on:

Seguence:

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APPLICANT: LIGHTON, OLD AND APPLICANT: LIGHTON, AND APPLICANT: LIGHTON, AND APPLICANT: JAMIESON, AND APPLICANT: JAMIESON, AND APPLICANT: JAMIESON, AND APPLICANT: JAMIESON, AND APPLICANTON: TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 8325-0020
CURRENT APPLICATION NUMBER: US/09/716,637
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: recognition OTHER INFORMATION: helix US-09-779-233-44
                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:SBS3 OTHER INFORMATION: recognition helix US-09-731-558-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 7; DB 4; Length 7; 100.0%; Pred. No. 3.8e+05;
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100.0%; Pred. No. 3.8e+05;
tive 0; Mismatches 0;
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US-09-779-233-44
; Sequence 44, Application US/09779233
; Patent No. 668958
; GENERAL INFORMATION:
; APPLICANT: Case, Casey
; TILE OF INVENTION: CELLS FOR DRUG DISCOVERY
; FILE REPERENCE: 8325-0010
; CURRENT APPLICATION NUMBER: US/09/779, 233
; CURRENT APPLICATION NUMBER: 201-02-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: EISENBERG, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%;
Conservative 0
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ORGANISM: Artificial Sequence
                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
7; Conserve
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1 RSDHLSR 7
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 7
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                                                                                                                                                                                                                            FEATURE:
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Sequence 49, Appl
Sequence 29, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 30, Appli
Sequence 30, Appli
Sequence 18, Appl
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Sequence 14, Application US/09731558
Patent No. 6503717
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
APPLICANT: Rebar, Edward J.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proceeding for the Identification of Gene Function
FILE REPERENCE: 019946-001321008
CURRENT APPLICATION NUMBER: US/09/731,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                            December 27, 2004, 20:31:09 ; Search time 16.35 Seconds (without alignments) 28.393 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-779-233-44
US-09-716-637-29
US-09-229-037-15
US-09-779-233-3
US-09-478-681-30
US-09-478-681-30
US-09-478-681-30
US-09-478-681-30
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length DB
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ORGANISM: Artificial Sequence
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Best Local Similarity
7; Conserve
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Sequence 15, Application US/09229037A

Sequence 15, Application US/09229037A

Sequence 15, Comment of C
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| Sequence 15, Application US/09478681 |
| Patent No. 6607882 |
| General Invormation: |
| APPLICANT: Case, Casey Christopher |
| APPLICANT: Case, Casey Christopher |
| APPLICANT: Bisenberg, Stephen P. |
| APPLICANT: Brancherg, Stephen P. |
| APPLICANT: Spratt, Sharon K. |
| TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS |
| TITLE OF INVENTION: USUGALATION OF SOURCE PROTEINS |
| FILE REFERENCE: 8325-0002.10 / S2-US3 |
| CURRENT FILING DATE: 200-01-06 |
| NUMBER OF SEQ ID NOS: 43 |
| SEQ ID NO 15 |
| LENGTH: 99 |
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-I F3
US-09-716-637-29
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                                                                                                                                                                                                               0; Indels
                                                                                                                                        Length 7;
                                                                                                                          100.0%; Score 7; DB 4; Le
nilarity 100.0%; Pred. No. 3.8e+05;
Conservative 0; Mismatches 0:
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Best Local Similarity 100...
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 99
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| Fateni No. 0534261
| Fateni No. 0534261bert
| APPLICANT: Case, Casey Christopher
| APPLICANT: Estanbarg, Stephen P.
| APPLICANT: Basenbarg, Stephen P.
| APPLICANT: Sangamo Biosciences, Inc.
| APPLICANT: Sangamo Biosciences, Inc.
| TITLE OF INVENTION: Regulation of Endogenous Gene Expression in Cells Using
| TITLE OF INVENTION: Zinc Finger Proteins
| TITLE REPREBENCE: 019496-002200US
| TITLE REPREBENCE: 10999-01-12
| NUMBER OF SEQ ID NOS: 40
| SEQ ID NOS: 40
| SEQ ID NO 30
| LENGTH: 196
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; OTHER INFORMATION: construct targeting upstream 9-base pair target; OTHER INFORMATION: site in VEGF promoter US-09-478-681-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: ZFP-VEGF1
US-09-779-233-3
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                                                                                                     Length 99;
                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 99;
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                                                                                                     100.0%; Score 7; DB 4; 100.0%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Case, Casey
TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REPERENCE: 8325-001.
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 3
LENGTH: 99
                                                                                                                                                      0; Mismatches
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; Sequence 3, Application US/09779233
; Patent No. 668958
; GNNERAL INFORMATION:
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US-09-478-681-30

| Sequence 30, Application US/09478681
| Patent No. 6607882
| GENERAL INFORMATION:
| APPLICANT: Cox III, George N. APPLICANT: Cox III, George N. APPLICANT: George N. APPLICANT: Spratt, Sharon F. APPLICANT: Spratt, Sharon F. TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS TITLE OF INVENTION: USING ZINC FINGER PROTEINS
| TITLE OF INVENTION: USING ZINC FINGER PROTEINS TITLE OF ENGRET FILING DATE: 2000-01-06
| CURRENT FILING DATE: 2000-01-06
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 30
| LENGTH: 196
| TYPE: PRT ORGANISM: Artificial Sequence FATURE INFORMATION: Description of Artificial Sequence: GEAURE: OTHER INFORMATION: 6-finger ZFP VEGF3a/1 from KpnI to BamHI US-09-478-681-30
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US-09-779-233-18
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Best Local Similarity 100.0%; Score 7; DB 4; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels
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100.0%; Score 7; DB 4; Length 196;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 7; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/09779233

Patent No. 6689558

GENERAL INFORMATION:

APPLICANT: Case, Casey

TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY

FILE REFERENCE: 8325-0010

CURRENT APPLICATION WUMBER: US/09/779,233

CURRENT FILING DATE: 2001-02-08

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 18

LENGTH: 196
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ORGANISM: Artificial Sequence
FEATURE:
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178 RSDHLSR 184
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